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SEARCH REQUEST FORM

Scientific and Technical Information Center

Mail Box and Bldg/Room Location	umber 30 <u>K 943</u> (M, 10E17 Res	Serial Number: 09/827937 ults Format Preferred (circle): PAPER-DISK E-MAI
If more than one search is submi	earch topic, and describe eywords, synonyms, acror hat may have a special m	as specifically as possible the subject matter to be searched. The subject matter to be searched.
= Title of Invention:	man G-1 Lietd	Priter coupel Receptor
Earliest Priority Filing Date:	5/7/97	parent, child, divisional, or issued patent numbers) along with the
depropriate sérial number. Wen Searl 550 10 NO		Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-308-3534
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STAFF USE ONLY Searcher:	Type of Search NA Sequence (#) /	Vendors and cost where applicable STN
Searcher Phone #: Searcher Location: Date Searcher Picked Up: 9/3 Date Completed: 9/9	AA Sequence (#)Structure (#)Bibliographic	Dialog
Searcher Prep & Review Time:	Fulltext Patent Family Other	Sequence Systems WWW/Internet Other (specify)

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Copyright

GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd

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Result
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Maximum Match 100%
Listing first 45 summaries
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Human P2-purinergi
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Human e-brotein co	G-protein	Human G-protein co	-	Human G protein-co	Human G-protein co	Amino acid sequenc	Amino acid sequenc	Human G protein co	novel G-p	CON215 G F	Human G-protein co	<u>.</u> ۾	G protein-c	Ç				Mouse 7-transmembr	. Rat KIAA0001 prote	Human UDP-glucose	č	G protein-	3		acid sec	Human HNEAA81 poly	G proteir	Human orphan G pro	Human 7-transmembr	n CON203 (human G pr	Human G protein co	Human chemokine re

ALIGNMENTS

RESULT AAW81576

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AAW81576;

22-FEB-1999

(first entry)

AAW81576 standard; Protein;

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EBV-induced G-protein coupled receptor; EBI-2; Epstein-Barr Virus; ulcer; endothelium-differentiation gene; EDG-1-like G-protein coupled receptor; recombinant; agonist; asthma; Parkinson's disease; heart fallure; asthma; hypotension; urinary retention; osteoporosis; antagonist; hypertension; angina pectoris; myocardial infarction; allergy; psychosis; depression; migraine; vomiting; stroke; eating disorder; migraine headache; cancer; prostatic hypertrophy; detection; drug screening.
          07-MAY-1997;
                                                                                                                          Misc-difference
                                  07-MAY-1998;
                                                         12-NOV-1998.
                                                                                   WO9850549-A2
                                                                                                                                                   Misc-difference
                                                                                                                                                               Key
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                   EBV-induced G-protein coupled receptor (EBI-2) polypeptide.
                                                                                                                     /note=
          97US-0852824
                                  98WO-US09048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc polypeptide. The encoding DNA is deposited under the accession number cc ATCC No: 209003. The invention provides two human G-protein coupled creceptor polypeptides. The polypeptides are human Estein-Barr Virus CC (EBV)-induced G-protein coupled receptor, designated EBI-2 polypeptide can a human endothelium-differentiation gene (EDG) like G-protein coupled receptor. Vectors CC comprising the EBI-2 and EDG-1-like G-protein coupled receptor. Vectors CC comprising the EBI-2 and EDG-1-like polypeptides encoding DNA can be used to transform host cells for the recombinant production of the proteins. CC Agonists for G-protein coupled receptors can be used for the treatment of CC asthma, parkinson's disease, acute heart failure, hypotension, uninary CC retention and osteoporosis. Antagonists can be used for the treatment of CC hypertension, angina pectoris, myocardial infarction, ulcers, asthma, CC allergies, psychoses, depression, migraine, vomiting, stroke, eating CC disorders, migraine headaches, cancer and benign prostatic hypertrophy.
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Best Local Similarity
Matches 342; Conser
 Human orphan
                                02-NOV-2000
                                                             AAY71306
                                                                                            AAY71306 standard;
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N-PSDB; AAV69760.
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                                                                                                                                                                                                                                                                                              efglvwheivnyicqvifwinflivivcytlitkelyrsyvrtrgvgkvprkkvnvkvfi
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                                (first entry)
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protein-coupled receptor hCHN8
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                                                                                            Protein;
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1 MQAVDNLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60

Query Match Best Local S Matches 342

Local Similarity nes 342; Conser

Conservative

0;

Score 1778; DB 21; Pred. No. 4.2e-187; ; Mismatches 0;

Indels Length

0;

0

DB 21;

100.0%;

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The present amino acid sequence is the hCHNB, an endogenous human corphan G protein-coupled receptor (GPCR), expressed in left and right cerebellum, kidney and lung. The hCHNB cDNA was identified using full length EST (expressed sequence tag) 764455 as a probe.

The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states.
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29-SEP-1999
21-CCT-1999
Sequence
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990S-0157280
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99US-0137127.
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identification of G protein-coupled
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28-MAY-1999;
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28-MAY-1999;
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28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
30-JUN-1999;
30-JUN-1999;
27-AUG-1999;
                                                                                                                    12-MAR-1999;
12-MAR-1999;
12-MAR-1999;
                                                                                                                                                                                   13-OCT-1998;
12-NOV-1998;
                                                                                                                                                                                                                                                                   Human; G protein coupled
identification; agonist;
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                                                                                                                                        12-MAR-1999;
12-MAR-1999;
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27-NOV-1998;
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990S-0123948.
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990S-0123949.
990S-0136436.
990S-0136437.
990S-0136437.
990S-0137127.
990S-0137127.
990S-0137131.
990S-0137567.
990S-0150525.
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99US-0120416.
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Matches 342
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                                                                        Human; G-protein-coupled receptor; GPCR; 15625 receptor protein; glial cells; spleen; colon; liver; brain; T-cell; heart; red cell; thymus; B-cell; pancreas; disorder; chromosome 3; anaemia; neutropenia; thrombocytopenia; gene therapy; ss.
Modified-site
                     Domain
                                Key
                                                      Homo
                                                                                                                                                         21-AUG-2000
                                                                                                                                                                                                    AAY94444 standard; protein;
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342; Conser
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rtial agonists useful as therapeutic age
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                                                                                                                   vectors to be used in gene therapy. The dolynucleotides using the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and polypeptides include anaemia, neutropenia and thrombocytopenia.
                                                                                                                                                                                               The present sequence shows the 15625 receptor protein. It is a novel G-coupled protein receptor (GPCR). The cDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues. The 15625 receptor protein may be useful for producing antibodies
                                                                                                                                                                                                                                                                                   Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anaemia, neutropenia and thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                               Sequence
                                                                                                                                                                     The 15625 receptor protein polynucleotides are useful probes, primers and antisense constructs. The polynuc
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25-AUG-1999;
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                                                                                                                                                                                       5625 receptor protein may be useful for producing antibodies can be used to detect the presence of the receptor protein.
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                                                                 Conservative
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99US-0382918.
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333..338
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163..165
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
The invention relates to polynuclootides (AAK51456-AAK53455) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating e.g. stem cell growth factor activity, haematopoiesis regulating
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15-SEP-2000;
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                                                                                                                                                                                                                                                                                                 AAE04386 standard; Protein; 342
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                                                                                                                                                  Human; P2-purinergic receptor; P2Y12; cardiant; vasotropic; thrompolytic; cerebroprotective; gynaecological; ADP; adenosine 5-diphosphate; angina; myocardial infarction; ischaemic attack; preeclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; vascular injury; schizophrenia; eating disorder; depression; angioplasty; peripheral vascular disease; platelet aggregation; restenotic; embolism; peripheral vascular stroke; pertussis toxin-sensitive G protein; thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein; c1; disseminated intravascular coagulation; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                        Human P2-purinergic receptor subtype, P2Y12.
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The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed CC as p2X12 receptor and its corresponding cDNA molecule. p2X12 receptor is expressed CC as presently principle receptor. The p2X12 receptor is expressed cc selectively in the platelets and brain, and couples to a pertussis toxin-cc selectively in the platelets and brain, and couples to a pertussis toxin-cc sensitive G protein (G1). p2X12 receptor is a G protein-coupled receptor cc sensitive G protein (G1). p2X12 receptor is a G protein-coupled receptor cc infarction, unstable angina, chronic stable angina, transient ischaemic ci infarction, unstable angina, chronic stable angina, transient ischaemic cc infarction, unstable angina, chronic stable angina, transient ischaemic cc thrombosis, embolism, disseminated intravascular coagulation, thrombotic ct thrombosis, embolism, disseminated intravascular coagulation, thrombotic cromplications or a bleeding disorder; thrombotic and cromplications or purpura or a bleeding disorder; vascular graft surgery, cc stent placements or insertion of endovascular devices and prostheses. Cc post CABG (coronary artery bypass graft) surgery, vascular graft surgery or paylic provides targets for screening cc diagnostic applications. P2X12 receptor provides targets for screening cc and other small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, vascular injury, or compound libraries to regulate platelet aggregation, vascular injury, or and other brain disorders. The present sequence is human p2-purinergic cand other brain disorders. The present sequence is human p2-purinergic crompound paylications paylications paylications paylications paylications paylications paylications.
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Sequence 342 AA;

Db	ОУ	Дb	Qy	рЬ	Qy	Вb	QΥ	В	Qy	Ма	Be	
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                                                                                                                                                                                 The 15625 receptor protein is a novel G-coupled protein receptor (GPCR). With sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in receptor protein is several other tissues. The 15625 receptor protein may be useful for receptor protein. The 15625 receptor protein may be useful for for generating probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor protein polynucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and present sequence is the macaque ortholog of the human 15625 receptor protein polynucleotides.
                                                                                                                                                                      Sequence
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                                           61
                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 90-92; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anaemia, neutropenia and thrombocytopenia
                                              Local Similarity
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25-AUG-1999;
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Macaque ortholog of human 15625 receptor protein
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                                                                                                                                                                                                                                                                                                 Homo sapiens.
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28-JUN-2001

26-DEC-2000; 23-DEC-1999; 2000WO-US34998 99US-0171622.

(CORT-) COR THERAPEUTICS INC.

Hollopeter G; Jantzen H, Ramakrishnan-Dubridge V,

N-PSDB; AAD08694. 2001-418082/44.

Example 1; Page 84-85; 108pp; English. Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, a for identifying binding partners and for diagnostic applications useful

The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed CC as P2X12 receptor and its corresponding cDNA molecule. P2X12 receptor is subtype of P2-purinergic receptor. The P2X12 receptor is electively in the platelets and brain, and couples to a pertussis toxin-CC sensitive G protein (Gi). P2X12 receptor is a G protein-coupled receptor is that responds to ADP. The invention also relates to a method for infarction, unstable angina, chronic stable angina; deep venous thrombosis, embolism, disseminated intravasscular coagulation, thrombotic customers by the model of thrombosis, embolism, disseminated intravasscular coagulation, thrombotic restenotic complications following angioplasty, carotid endarterectomy, post CABG (coronary artery bypass graft) surgery, vascular graft surgery,

뫄 Ş В Ş

88888888888

Hollopeter G;

2001-418082/44.

Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications

for identifying binding partners and for diagnostic

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RESULT
AAE04384
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Best Local Sim
Matches 315;
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                                                                                                                                                                                                                   Rat; P2-purinergic receptor; P2Y12; cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5' diphosphate; angina; myocardial infarction; ischaemic attack; preeclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angioplasty; peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein; c1; disseminated intravascular coagulation; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                      Rat P2-purinergic receptor subtype, P2Y12.
                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE04384 standard;
                                                                                                            28-JUN-2001
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(CORT-) COR THERAPEUTICS INC
                                    23-DEC-1999;
                                                                         26-DEC-2000;
                                                                                                                                                 WO200146454-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                           2000WO-US34998
                                    9908-0171622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.9%; Score 1634; DB 22; 100.0%; Pred. No. 2.6e-171;
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Conley PB,

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Ramakrishnan-Dubridge V,

Julius 5

RESULT 1
AAY94498
ID AAY9
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AC AAY9
AC AAY9
XX 15-S
XX
DE Rat

AAY94498

standard;

protein; 387

15-SEP-2000

(first entry)

Rat MP-10 receptor protein

20 В ð 멍 Ş В δÃ

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The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed composed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is corresponding cDNA molecule. P2Y12 receptor is expressed consistively in the platelets and brain, and couples to a pertussis toxing sensitive grotein (Gi). P2Y12 receptor is a grotein-coupled receptor conference which is useful for modulating acute myocardial confertifying an agent which is useful for modulating acute myocardial conference which is useful for modulating acute myocardial conference who is a chronic stable angina, transient ischaemic conference who is a chronic stable angina, transient ischaemic conference who is a chronic stable angina, transient ischaemic conference who is thrombosis, peripheral vascular disease, preeclampsia, deep venous conference complications following angioplasty, carotid endarterectomy, constituted complications following angioplasty, carotid endarterectomy, constituted articles and conference and prostheses. The present graft surgery, vascular graft surgery, stent placements or insertion of endovacular devices and prostheses. Compound libraries to regulate platelet aggregation, vascular injury, or compound libraries to regulate platelet aggregation, vascular injury, or and other brain disorders. The present sequence is rat P2-purinergic conference as the prosteried as P2Y12 receptor.
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Best Local S
Matches 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                  186 WHEIVNYICOVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVF
                                                                                                                                                                                 132
                                                                                                                                                                                                            126
                                                                                                                      192
 312
                                                           252
                           306 RNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 342
                                                                                                                                                                                                                                                                                                     12
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                                                                                                                                                                                                                                     wheivnyicqvifwinflivivcyslitkelyrsyvrtrgsakapkkrvnikvfiiiavf
                                                                                                                                                                                                                                                                                                                                                                  293;
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         343
                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                Score 1528.5; DB 2
Pred. No. 1.2e-159;
7; Mismatches 22;
    343
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 287
                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is rat MP-10 receptor protein. The DNA encoding this protein was identified from a rat brain stem/spinal cord cDNA library. In situ hybridisation analysis showed that MP-10 receptor mRNA is expressed diffusely but ubiquitously in the adult rat central mervous system (CNS). The mRNA was also found in adult rat spleen. MP-10 receptor protein contains several structural features characteristic of a G protein coupled receptor (GPCR). MP-10 receptor protein is useful for identifying new anaesthetic and analgesic agents. Such agents may be identified using assays designed to detect agonists or antagonists capable of binding to the receptor, in therefore modulating intracellular signalling.
                                                 312
                                                                        306
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                           246
                                                                                                                                                    192
                                                                                                                                                                            186
                                                                                                                                                                                                    132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel G protein-coupled receptor, MP-10 receptor, useful identification of new anaesthetic and analgesic agents -
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(ASTR ) ASTRA AB.
                                                                                                                                                                                                                            126
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                                                                                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                               6
                                                                  RNSLISMLKCPNSATSLSQDNRKKEQDGGDPN 337
                                                                                                                                         WHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVF
                                                                                                      FICFVPEHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDDFIYFFLCKSF
                                                                                         {\tt ficfvpfhfaripytlsqtravfdcnaentlfyvkestlwltslnacldpfiyfflcksf}
                                                                                                                                                                                           {\tt ttrpfktsspsnllgakilsvaiwafmfllslpnmiltnrrpkdkditkcsflksefglv}
                                                                                                                                                                                                                                                                                            NLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLKN 65
                                                                                                                                                                                                        TTRPPKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSPLKSEFGLV 185
                                                                                                                                                                                                                                                          TVISDLLMILTEPEKILSDAKLGTGPLRTEVCQVTSVIFYFTMYISISELGLITIDRYQK 125
                                                                                                                                                                                                                                            tvisdllmiltfpfkilsdaklgaghlrtlvcqvtsvtfyftmyisisflglitidrylk
                                                                                                                                                                                                                                                                                                                                                       287; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  387 AA;
                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98SE-0004274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor; GPRC; MP-10 receptor; rat;
ystem; spleen; anaesthetic; analgesic.
                                                                                                                                                                                                                                                                                                                                                                  84.0%;
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                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                               Score 1493.5; DE
Pred. No. 1e-155;
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                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Donnell D,
                                             338
                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length
                                                                                                                                                                                                                                                                                                                                                  23;
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The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed CC as P2712 receptor and its corresponding CDNA molecule. P2712 receptor is captered to the subtype of P2-purinergic receptor. The P2712 receptor is expressed CC selectively in the platelets and brain, and couples to a pertussis toxin CC sensitive G protein (Gi). P2712 receptor is a G protein-coupled receptor CC that responds to ADP. The invention also relates to a pertussis toxin CC identifying an agent which is useful for modulating acute myocardial CC infarction, unstable angina, chronic stable angina, transient ischaemic CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic cthrombosis, embolism, disseminated intravascular coagulation, thrombotic CC thromboytopaenic purpura or a bleeding disorder; thrombotic and CC restenotic complications following angioplasty, carotid endarterectomy, CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery, CC stent placements or insertion of endovascular devices and prostheses. CC P2712 receptor is useful for identifying binding partners and for CC disease as well as schizophrenia, eating disorders, depression, migraine CC compound libraries to regulate platelet aggregation, vascular injury, or Cdisease as well as schizophrenia, eating disorders, depression, migraine CC receptor subtype, P2712 truncated allelic variant. The variant is CC obtained by deleting two bases 'CA' from position 789-790 of the wildtype human P2712 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 29; Page 91-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan; 'z'-purinergic receptor; P2Y12; cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; preeclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migralne; vascular injury; schizophrenia; eating disorder; depression; angioplasty; peripheral vascular disease; platelet aggregation; restenotic; embolism; cl; disseminated intravascular coagulation; thrombosis; mutant; mutein; variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-418082/44.
DB; AAD08700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P2-purinergic receptor subtype, P2Y12 truncated allelic variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P2-purinergic receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jantzen
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Query Match Best Local Similarity Matches 242; Conser

Conservative

95

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Score 1237.5; Pred. No. 9.4 ed. No. 9.4 Mismatches

Length

267;

Gaps

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267

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                                                                                                                                                                                                                                                                                                                                                                                                                                   skin disorder; cardiovascular disorder; atherosclerosis; restenosis; neurological disease; Alzheimer's disease; trauma; wounding; spinal cord injury; skeletal disorder; cytostatic; immunosuppressive; anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic; neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant; dermatological; gene therapy.
          Sequences AAB23029-B23048 represent human SECX proteins. The SEQX proteins of the invention are either secreted or membrane-associated proteins and act as regulator of ceillular proliferation and differentiation. SECX proteins or nucleotides are useful for diagnos,
                                                                                                             Novel human membrane associated or secreted polypeptides and polynucleotides useful for diagnosis, prevention and treatment pathological states such as cancer, immune, cardiovascular and neurological disorders
                                                                                                                                                                                                                                                                                  09-MAR-1999; 99US-0123667
08-MAR-2000; 2000US-0123667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECX protein; human; secreted; membrane-associated; cancer; proliferation regulator; differentiation regulator; non-malignant tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB23029 standard; Protein; 333
                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                           09-MAR-2000; 2000WO-US06280
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune disorder; autoimmune disease; transplant rejection; allergy; AIDS; infection; inflammatory disorder; arthritis; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2001
                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .mmune disorder;
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presence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemokine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 155;
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Best Local
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313 rkttassgenhssgtd
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                                                                       NSATSLSQDNRKKEQD
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                                                                           332
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Pred. No. 1.1e-82;
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17-AUG-1999;
            27-FEB-2001
                     JP2001054389-A.
    99JP-0230777
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Human; G protein

coupling receptor;

CNS; central nervous system

Human G protein coupling receptor.

11-JUL-2001

(first

entry)

AAB74397 ID

AAB74397 standard;

Protein; 333

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Best Local S
Matches 155
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   23-JUL-1999;
                                                                           23-JUL-1999;
                                                                                                                                                  06-FEB-2001.
                                                                                                                                                                                                                          JP2001029083-A.
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                       Ниman;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human
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Pred. No. 1.1e-82;
7; Mismatches 102
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Human; G protein-coupled receptor; GPCR; CON203 protein; schizophrenia; neuroleptic; nootropic; neuroprotective; bipolar disease; psychotropic; neurological disorder; psychitric citisease; neurist; neuritis; attention deficit hyperactivity disorder; neurasthenia; senile dementia; affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease depression; migraine; genetic screening; chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                           Human CON203 G protein-coupled receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences for a novel human G protein coupled receptor. This is useful in the identification of treatments for central nervous system diseases such schizophrenia, Parkinson's disease and aches.
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                 their corresponding DNA molecules. GPCR is also referred as seven transmembrane receptor. G protein coupled receptor protein is useful for treating neurological disorder, particularly schizophrenia. GPCR protein is also useful for identifying compounds useful for treating other schizophrenia. These compounds are also useful for treating other neurological and psychiatric diseases, e.g. depression, anxiety, bipolar disease, affective disorders, attention deficit hyperactivity disorder/ attention deficit disorder, epilepsy, neuritis, neurostathenia, neuropathy, neurostas, Alzheimer's disease, Parkinson's disease, migraine and senile dementia. The invention also provides genetic screening procedures that entail analysing a person's genome with respect to GPCR. The vectors are useful for the recombinant production of the GPCR's. The present sequence is human GNNATA correction.
                                                                                                                                                                                                                                         Seven transmembrane receptor polypeptides and polynucleotides, useful for treating neurological or psychiatric disorders, e.g. schizophrenia as well as for identifying compounds useful for treating schizophrenia
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                                                                                                                                                                               The invention relates
                                                                                                                                                                                                         Claim 1; Page 10-11;
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Copyright (c) 1993 - 2000 Compugen
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ALIGNMENTS

A;Note: the authors translated the codon AAT for residue 316 as Lys R;Seyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W. Genomics 13, 832-834, 1992
A;Title: The human platelet-activating factor receptor gene (PTAFR) contains A;Reference number: A42831; MUID:92347886
A;Accession: A42831 RESULT A40191 A; Molecule type: DNA
A; Residues: 1-226, 'TG', 229-342 <SBY>
A; Residues: 1-226, 'TG', 229-342 <SBY>
A; Cross-references: GB: M88177; NID: g190697; PIDN: AAA60214.1;
A; Note: sequence extracted from NCBI backbone (NCBIN: 109813, A; NCBI: Sequence extracted from NCBI backbone (NCBIN: 109813, A; NCBI: Sequence (A;Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID R;Sugimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Biochem. Biophys. Res. Commun 189, 617-624, 1992
A;Title: Molecular cloning and characterization of the platelet-activating A;Reference number: JC1359; MUID:93112021
A;Accession: JC1359 A;Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538 A;Experimental source: granulocyte, cell line HL-60 all R;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.; Minami, M.J. Biol. Chem. 266, 20400-20405, 1991
A;Title: Molecular cloning and expression of platelet-activating factor A;Reference number: A41079; MUID:92041873 R;Kunz, D.; Gerard, N.P.; Gerard, C. J. Biol. Chem. 267, 9101-9106, 1920. A;Title: The human leukocyte plateLet-activating factor receptor. cDNA cloning, A;Reference number: A40191; MUID:92250505 platelet-activating factor receptor - human C;Species: Homo sapiens (man) C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change C;Accession: A40191; JH0479; A41079; JC1359; A42831; I51923 A;Cross-references: GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:g456294 R;Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G. Biochem. Biophys. Res. Commun. 180, 105-111, 1991 A;Title: Characterization of a human cDNA that encodes a functional rece A; Molecule type: mRNA A; Residues: 1-342 < KUN> A;Reference number: JH0479; MUID:92028922 A;Accession: JH0479 A; Experimental source: heart A; Molecule type: mRNA A; Residues: 1-315,'N',317-342 <SUG> A; Molecule type: mRNA A; Residues: 1-342 <NAK> A;Status: not compared with conceptual translation A;Molecule type: mRNA A; Accession: A41079 A; Molecule type: mRNA A; Residues: 1-342 <YER> A; Accession: A40191 a functional receptor for plat H.; Minami, M.; Bito, PID:g190698 NCBIP:109814) 20-Jun-2000 factor receptor from PID: g219976 factor rec no cell intro H . ;

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A;Status: prelimin..
A;Molecule type: DNA
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^~oss-references: GB:S'
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A;Map position: 1935-1934.3
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;17-38/Domain: transmembrane #status predicted <TII>F;24-75/Domain: transmembrane #status predicted <TII>F;92-113/Domain: transmembrane #status predicted <TIV>F;133-4155/Domain: transmembrane #status predicted <TV>F;184-205/Domain: transmembrane #status predicted <TV>F;233-253/Domain: transmembrane #status predicted <TV>F;233-253/Domain: transmembrane #status predicted <TVI>F;237-297/Domain: transmembrane #status predicted <TVI
                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-342 <HON>
A;Cross-references: GB:X56736; NID:g49442; PIDN:CAA40060.1; PID:g49443*
A;Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                     R:Honda, Z.; Nakamura, M.; Miki, I.; Minar Nature 349, 342-346, 1991
A:Title: Cloning by functional expression A; Reference number: S13638; MUID:91101726
A; Accession: S13638
                                                                                                                                                                                                                                                                                                                      platelet-activating factor receptor - guinea
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar
C;Accession: S13638
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S13638
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  Query Match
Best Local S
Matches 103
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Best Local Similarity 32.6
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    Local Similarity
nes 103; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYF
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  22.1%;
llarity 30.7%;
Conservative (
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      66;
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Pred. No. 1.6e-26;
1; Mismatches 134
  Score 392.5; DB 2;
Pred. No. 2.1e-26;
5; Mismatches 146;
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                                                                                                                                                                                                                                                            of platelet-activating factor receptor from g
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                                     DB 2;
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A;Title: Epstein-Barr virus-induced genes:
A;Reference number: A45680; MUID:93188173
A;Accession: B45680
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845680

G protein-coupled peptide receptor C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revis C:Accession: B45680
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                                                            В
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A; Residues: 1-361 <BIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Birkenbach, M.; Josefsen, K.;
J. Virol. 67, 2209-2220, 1993
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Best Local S
Matches 94
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                      282
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                    STLWLTSLNACLDPFIYFFLCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETP
                                                                                                                                                                                                                                                            SISFLGLITIDRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMI--LTNRQPR 168
                                                            SGVNK---KALNT-TILITYVFVLCFTPYHVAIIQHMIKKLRESNFLECSQRHSFQISLH 291
                                                                                                 RGVGKVPRKKVNVKVFIIIAVFFICFVPFHFARIPYTLSQTR--DVFDCTAENTLFYVKE
                                                                                                                                                                               DKNVKKCSFLKSEFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRS-----YVRT
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                                                                                                                                                                                                                                                                                                                                           SN-FIIFLKNTVISDLLMILTFPFKIL-----SDAKLGTGPLRTFVCQVTSVIFYFTMYI 110
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Kieff,

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protein-couple

PID:g292057 NCBIP: 127097)

Indels Length

Gaps

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R.Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, Blochem. J. 314, 671-678, 1996
A;Title: A murine platelet-activating factor 1
A;Reference number: S63666; MUID:96239129
A;Accession: S63666
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995
C;Accession: 843252
C;Accession: 843252
R;BltO, H; Honda, Z.; Nakamura, M.; Shimizu, T.
R;BltO, H; Honda, Z21, 211-218, 1994
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A; Cross-references: EMB
C; Superfamily: ATP rece
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                                                     A; Molecule type: mRNA
A; Residues: 1-341 <BIT>
A; Cross-references: GB:
C; Superfamily: ATP rece
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                                                                                                                            A; Title: Cloning, expression and tissue distribution A; Reference number: S43252; MUID:94222063
                                                                                                              A; Accession: S43252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local s
Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: S63666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Mus musculus (house mouse)
Date: 28-Oct-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :Cross-references: EMBL:D50872; NID:g1256924; Superfamily: ATP receptor P2u
Query Match
Best Local Similarity
                                                        Cross-references: GB:U04740;
Superfamily: ATP receptor P2u
                                                                                                                                                      to, H.; Honda, Z.; Nakamura, M.; Shimizu, J. Biochem. 221, 211-218, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQI--RSKSNFI-IFLKNTVISDLLMILT
                                                                                                                                                                                                                                                                                                       HLSEKFYSMRSSRKC-SRATS
                                                                                                                                                                                                                                                                                                                                                                  CFVPHHVVQLPWTLAELG - - YQTNFHQAINDAHQITLCLLSTNCVLDPVIYCFLTKKFRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLLGAKILSVVIWAFM-----FLLSLPNMILTNRQPRDKNVKKCSFLKSEFG----LVWHE
                                                                                                                                                                                                                                                                                                                                      ----SLISMLKCPNSATS 321
                                                                                                                                                                                                                                                                                                                                                                                             CEVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRN
                                                                                                                                                                                                                                                                                                                                                                                                                         FIAFCFFLVFFLIFYCNLVIIHTLLTQPMRQQ--RKAGV----KRRALWMVCTVLAVFII
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28
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Pred. No. 4.1e-24;
 Score
Pred.
                                                                      :9470384;
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   362;
   ; DB 2;
9e-24;
                                                                        PIDN:AAA18422
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               Length 341;
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                                                                         PID:g470385
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A; Residues: 1-308 <WEB>
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                              14 TSLCTRDYKITQVLFPLLYTVLFEVGLITNGLAMRIF-FQIRSKSNFIIFLKNTVISDLL
                                                                              Local
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       SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLL
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                                                                87; Conser
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G protein-coupled receptor 6H1 - chicken N;Alternate names: purinoceptor 6H1 C;Species: Gallus gallus (chicken) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000 C;Accession: I50241; JC4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kaplan, M.H.; Smith, D.T.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled
A;Reference number: I50241; MUID:93329058
                                                                                                                  A;Gene: p2Y5
C;Superfamily: ATP receptor P2u
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane |
E;15-40/Domain: transmembrane #status predicted <TM1>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A; Title: Identification of 6H1 as a P2Y purinoceptor:
A; Reference number: JC4618; MUID:96190677
F;133-153/Domain: transmembrane #status predicted <TM4>F;177-201/Domain: transmembrane #status predicted <TM5>F;277-248/Domain: transmembrane #status predicted <TM6-F;269-292/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLLGAKILSVVIWAFM-----FLLSLPNMILTNRQPRDKNVKKC-----
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                                                                                                                                                                                                                                                                                                                             nces: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384 source: T-cells receptor plays a role in T-cell activation.
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20.1%;

Score 357.5; DB Pred. No. 2e-23; 8; Mismatches 12

125; 2;

15;

Gaps

8

62

Length Indels

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intron 17 purinergic receptor p275
N;Alternate names: G-protein couple
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revis
C;Accession: T09508
R;Bohm, S.K.; Trumpp, A.; Khitin, I
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C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S15403
R;Sasaki, K: Yamano, Y: Bardhan, S:: Iwai, N:: Murray, J.J.; Hasegawa, M.; Matsuda, Y.
Reture 351, 230-233, 1991
A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiote
A:Reference number: S15403; MUID:91251900
A:Accession: S15403
A:Status: preliminary
A:Molocula +ruce. menn
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A;Residues: 1-359 <SAS>
A;Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1;
C;Superfamily: vertebrate rhodopsin
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S15403
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         Accession: T09508
Bohm, S.K.; Trumpp,
                                Species: Homo sapiens (man)
Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 95
                                                                                                                                                                                  313 FLQLLKYIPPKAKSHSNLSTKMSTLSYRPSENGNSSTKKP
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                                                                                                                                                                                                                  LISMLK-CPNSATSLSQDNRK-----KEQDGGDPNEETP 341
                                                                                                                                                                                                                                                 WVPHQIFTFMDVLIQLGLIRDCKIEDIVDTAMPITICLAYFNNCLNPLFYGFLGKKFKKY
                                                                                                                                                                                                                                                                                                                                                                                      CIIIWLLAGLASLPTIIHRNVFFIENTNITVCAFHYESQNSTLPVGLGLT-KNILGFL--
                                                                                                                                                                                                                                                                                                                                                                                                                       SYVIWAFMFLLSLPNMILTN-RQPRDKNVKKCSF------LKSEFGLVWHEIVNYICQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLFPLLYTVLFFVGLITNGL-AMRIFFQIRSKSNFIIFLKNTVISDLLMILTFPFKILSD
                                                                                                                                                                                                                                                                               RIPYTLSQTRDVF-----DCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNS 308
                                                                                                                                                                                                                                                                                                                   ----FPFLIILTSYTLIWKTLKKAYEIQK---NKPRKDDIFKIILAIVLFFF-----FS
                                                                                                                                                                                                                                                                                                                                                    VIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVPFHFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAIVHPMKSRLRRTMLVAKVT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVPYNITLILYSLMRTQTWINCSVVTAVRTMYPV---TLCIAVSNCCFDPIVYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVFTLPFRIYYFV-VRNWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVPFHFARIPYTLSQTRDVFDC---TAENTLFYVKESTLWLTSLNACLDPFIYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQ-NNTEQRTCFENFPESTWKTYLSR
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            A.; Khitin,
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27.9%;
                                                                             coupled
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         L.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 339; DB 2;
Pred. No. 9.2e-22;
                                                                             receptor
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       Kong,
         ∑
       Payan,
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       D.G.;
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Bunnett,
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       Z
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C; Accession:
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A;Residues: 1-359 <RES>
A;Cross-references: GB:D13814; NID:g471120; PIDN:BAA02968.1; PID:g471121
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                   A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                   angiotensin II receptor type 1b
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_re
C;Accession: I39418
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
I39418
                                                                                                                                                                                                                                                                                          A; Accession: I39418
                                                                                                                                                                                                                                                                                                     A; Reference number:
                                                                                                                                                                                                                                                                                                                        Biochem. Biophys.
A; Title: Novel sul
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C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z16705
A;Accession: T09508
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A; Residues: 1-344 < BOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, A;Description: The human purinergic
                                                                                                                                   Matches
                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 87
      89
                                                                     29
                                                                               299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 RNSLISMLKCPNSATSLSQDNRKKEQDGGD
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                          AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
AMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAIVHPMKSRLRRTMLVAKVT
                                                             VMTPTLYSIIFVVGIFGNSLVVIVIYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNS----IKMKNWSVRRS-DFRFSEVHGAE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVPYNINLILYSLVRTQTFVNCSVVAAVRTMYPI---TLCIAVSNCCFDPIVYYFTSDTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVIFIEIVGFFIPLILNVTCSSMVLKTLTKPVTLSR--SKINKTKVLKMIFVHLIIFCFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVPFHFARIPYTLSQTRDVFDCT---AENTLFYVKESTLWLTSLNACLDPFIYFFLCKSF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFIC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKC---SFLKSEFGLVWHE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEVETLPERIEY-FTTRNWPFGDLLCKISVMLEYTNMYGSILFLTCISVDRFLAIVYPEK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFF-QIRSKSNFIIFLKNTVISDL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKTLRTKRNAKIVCTGVWLTVIGGSAPAVFVQSTHSQGNNASEACFENFPEATWKTYLSR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMILTEPEKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSSHCFYNDSFKYTLYGCMFSMVFVLGLVSNCVAIYIFICVLKVRNETTTYMINLAMSDL
                                                                                                                                                Similarity
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87; Conservative
                                                                                                                                                                                                                                                                                                     ys. Res. Commun. 199, 467-474, 1994 subtype of human angiotensin II type beer: I39418; MUID:94183213
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                #sequence_revision 29-May-1998 #text_change 24-Nov-1999
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                                                                                                                                             18.5%;
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                                                                                                                               58;
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                                                                                                                              Score 329; DB 2;
Pred. No. 6.7e-21;
8; Mismatches 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 338; DB 2;
Pred. No. 1.1e-21;
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                                                             88
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proteinase activated receptor 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C:Accession: 148705
R:Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.
J. Biol. Chem. 270, 5950-5955, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiotensin II receptor type 1 - dog
(Species: Canis lupus familiaris (dog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-No
C;Accession: $44425
R;Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FEBS Lett. 343, 146-150, 194
                                                                                                                          RESULT
148705
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A;Molecule type: mRNA
A;Residues: 1-359 <BUR>
A;Cross-references: PIDN:AAB30674.1;
A;Experimental source: liver
C;Superfamily: vertebrate rhodopsin
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Best Local Similarity 29.2
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145
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                                                                                                                                                                                                        YIPPKAKSHSSLSTK
                                                                                                                                                                                                                                                                                                                                                                   ----FPFLIILTSYTLIWKTLKRAYEIQK---NKPRNDDIFKIIMAIVLFFFFSWVPHQI 258
                                                                                                                                                                                                                                                                                                                                                                                          VIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFI-IIAVFFICFVPFHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVVIWAFMFLLSLPNMILTN-RQPRDKNVKKCSF------LKSEFGLVWHEIVNYICQ 195
                                                                                                                                                                                                                                              -CPNSATSLSQDNRK 328
                                                                                                                                                                                                                                                                                                                      ARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLISMLK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIIIWLLAGLASLPTIIHRNVFFIENTNITVCAFHYESQNSTLPIGLGLT-KNILGFL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYVAIVHPMKSPVRRTMLMAKVT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VMIPTLYSIIFVVGIFGNSLVVIVIYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLFPLLYTVLFEVGLITNGL-AMRIFFQIRSKSNFIIFLKNTVISDLLMILTFPFKILSD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LISMLK-CPNSATSLSQDNRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIPYTLSQTRDVF-----DCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIIIWLLAGLASLPAIIHRNVFFIENTNITVCAFHYESRNSTLPIGLGLTKNILGS--C-
                                                                                                                                                                                                                                                                                      FTFLDVLIQLGIIHDCKIADIVDTAMPITICIAYFNNCLNPLFYGFLGKKFKKYFLQLLK 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----FPFLIILTSYTLIWKALKKAYEIOK---NNPRNDDIFRIIMAIVLFFF-----FS
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29.2%; Pred. No. 1.2e-20;
tive 54; Mismatches 147;
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A;Cross-references: GB:S59041; NID:g299614; PIDN:AAB26239.1; PID:g299615
A;Experimental source: proximal tubule cells
A;Experimental source: proximal tubule cells
A;Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBIP:12960:
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                               R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A;Title: Cloning of a rabbit kidney cortex
A;Reference number: A48857; MUID:93236091
A;Accession: A48857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiotensin II receptor type 1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning A;Reference number: 148705; MUID:95197620
A;Accession: 148705
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-399 <RESS
A;Cross-references: EMBL:248043; NID:g663020; PIDN:CAA88097.1; PID:g663021
C;Superfamily: ATP receptor P2u
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A; Residues: 1-359 <BUR>
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                                                                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity 27.6
Matches 92; Conservative
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AMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAIVHPMKSRLRRTMLVAKVT
                                  AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL
                                                                      VMIPTLYSIIFVVGIFGNSLAVIVIYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGVFLFPALLTASAYVLMIKTLRSSAMDEHSEKK--RORAIRLIITVLAMYFICFAPSNL
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                                                                                                                                                Conservative
                                                                                                                                                              18.3%;
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27.6%;
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                                                                                                                                                                Score 325;
Pred. No. 1
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Pred. No. 1.5e-20;
3; Mismatches 141;
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SVVIWAFMFLLSLPNMILTN-RQPRDKNVKKCSF---

-- LKSEFGLVWHEIVNYICQ

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angiotensin II receptor type 1 - human
N;Alternate names: angiotensin II receptor IA
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
C;Accession: JC1104; JQ1402; JH0574; JH0267; A44014; S18983
R;Mauzy, C.A.; Hwang, O.; Egjoff, A.M.; Wu, L.H.; Chung, F.Z.
Biochem. Biophys. Res. Commun. 186, 277-284, 1992
A;Title: Cloning, expression, and characterization of a gene enc.
A;Reference number: JC1104; MUID:92337608
                                                                                                                                                                                                                                                                                              A;Experimental source: liver
R;Curnow, K.M.; Pascoe, L; White, P.C.
Mol. Endoctinol 6, 1113-1118, 1992
A;Title: Genetic analysis of the human type-1
A;Reference number: A44014; MUID:92375105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z11162; NID:g28709; PID:g28710
A;Experimental source: lymphocyte
R;Bergsma, D.J.; Ellis, C.; Kumar, C.; Nuthulaganti, P.; Kersten, H.; Elshourbagy,
Biochem. Biophys. Res. Commun. 183, 989-995, 1992
A;Title: Cloning and characterization of a human angiotensin II type 1 receptor.
A;Reference number: JH0574; MUID:92231907
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A; Map position: 3q21-3q25
C; Superfamily: vertebrate
C; Keywords: G protein-coup
F; 30-53/Domain: transmemb
                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-359 < CUR>
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-359 < TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Molecular cloning, sequence analysis and A;Reference number: JH0267; MUID:92198490 A;Accession: JH0267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Takayanagi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Haji, M.; Inagami, Biochem. Biophys. Res. Commun. 183, 910-916, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-359 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JH0574
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A: Residues: 1-359 <FUR>
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Biochem. Biophys. Res. Commun. 183, 8-13,
A; Title: Molecular cloning and sequencing
A; Reference number: JQ1402; MUID:92181475
A; Accession: JQ1402
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                                                                                                                  A; Gene: GDB: AGTR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: liver
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                   Superfamily: vertebrate rhodopsin Reywords: G protein-coupled recen
                                                                                                                                                             Cross-references: GB:M93394; NID:g178680; PID:g178681: Note: sequence extracted from NCBI backbone (NCBIN:11
                                                                                            Cross-references: GDB:132359; OMIM:106165
                                                                                                                                                                                                                                                     Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CPNSATSLSQDNRK
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  protein-coupled
n: transmembrane
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receptor; glycoprotein;
#status predicted <TM1>
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of the gene encoding
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                          hormone
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                                                                                                                                                                NCBIP: 111833)
                          receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-370 <JAN>
A; Cross-references: DDBJ:AF005419;
C; Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heptahelical P2Y5-like receptor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change C;Accession: JC5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D. Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A;Title: Cioning of a human heptabelical receptor closely
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                                                                                                                                                                                                                                   LGNATANNT-CIVDDSFKYNLNGAVYSVVFILGLITNSVSLFVFCFRMKMRSETAIFITN
                                                                                                                                                                                                                                                                             LTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIF-FQIRSKSNFIIFLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LISMLK-CPNSATSLSQDNRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WIPHQIFTFLDVLIQLGIIRDCRIADIVDTAMPITICIAYFNNCLNPLFYGFLGKKFKRY 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIPYTLSQTRDVF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVPFHFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIIIWLLAGLASLPAIIHRNVFFIENTNITVCAFHYESQNSTLPIGLGLT-KNILGFL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVVIWAFMFLLSLPNMILIN-ROPRDKNVKKCSF-----LKSEFGLVWHEIVNYICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMIPTLYSIIFVVGIFGNSLVVIVIYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYT
                      --VWHEIVNYICQVIFWINFLIVIV---
                                                              IVYPFRSRTIRTRRNSAIVCAGVWILVLSGGISASLFST---
                                                                                                        TTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGL-
                                                                                                                                                   LAVSDLLEVCTLPFKIFYNEN-RHWPFGDTLCKISGTAFLTNIYGSMLFLTCISVDRFLA
                                                                                                                                                                                         TVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----FPFLIILTSYTLIWKALKKAYEIQK---NKPRNDDIFKIIMAIVLFFF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL
                                                                                                                                                                                                                                                                                                                          87;
                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                            18.1%; 27.7%;
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28.7%;
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                                                                                                                                                                                                                                                                                                                          67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 321; DB
Pred. No. 3.3e-
56; Mismatches
                                                                                                                                                                                                                                                                                                                                            Score 321; DB 2;
Pred. No. 3.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g2240034;
                                                                                                                                                                                                                                                                                                                          Mismatches
-CYTLITKELYR----
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3.3e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN: AAB66322.1;
                                                                  --TNVNNATTTCFE-GLS
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  SYVRTRGVGKVPRKKV
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4

Job time: 130 sec

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A; Molecule type: mRNĀ
A; Residues: 1-359 <IMAA
A; Residues: 1-359 <IMAA
A; Cross references: GB:X64052; NID:g57521; PIDN:CAA45410.1; PID:g57522
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: S20423; MUID:92183879
A;Accession: S20423
A;Status: preliminary
A;Molecule turns of two subtypes in the rat type I angiotensin II receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiotensin II receptor type 1B (AT3) - rat
N;Alternate names: angiotensin II receptor chain B
C;Species: Rattus norvegicus (Norvay rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A42656; S20423
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J. Biol. Chem. 267, 9455-9458, 1992
A;Title: Cloning and expression of a novel angiotensin II receptor subtype A;Reference number: A42656; MUID:92250585
A;Accession: A42656
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A; Residues: 1-359 <SAN>
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Matches 92
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                                                                                                                                                                                                                                                                    196 VIFWINELIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVF-IIIAV---FFICEVP 251,
                                                                                                                                                                                                                                                                                                                     149 CIIIWLMAGLASLPAVIYRNVYFIENTNITVCAFHYESQNSTLPIGLGLT-KNILGFV---: 205
                                                       312 MLK-CPNSATS 321
                                                                                                                                                                                                                206 ----FPELIILTSYTLIWKALKKAYKIQK---NTPR---NDDIFRIMAIVLFFEFSWVP 255
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316 LLKYIPPTAKS 326
                                                                                                           256 HQIFTFLDVLIQLGIIRDCEIADIVDTAMPITICIAYFNNCLNPLFYGFLGKKFKKYFLQ 315
                                                                                                                                                                                                                                                                                                                                                                                     145 SVVIWAFMFLLSLPNMILTNRQ-PRDKNVKKCSF-----LKSEFGLVWHEIVNYICQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 PFIYFFLCKSFRNS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 LKMITVHMAVFVVCFVPYNSVLFLYALVRSQAITNCFLERFAKIMYPITLCLATLNCCFD 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 KRVWKTYLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRKPATLSQIGTN-----KKKV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 VLFPLLYTVLFFVGLITNGL-AMRIFFQIRSKSNFIIFLKNTVISDLLMILTFPFKILSD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                                                                         AMEYRWPEGNHLCKIASASVSENLYASVELLTCLSIDRYLAIVHPMKSRLRRTMLVAKVT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMIPTLYSIIEVVGIEGNSLVVIVIYEVMKLKTVASVELLNLALADLCELLTLPLWAYYT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVKVFIIIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLD 294
                                                                                                                                                         FHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLIS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.9%; Score 319; DB 2; Length 359; 29.6%; Pred. No. 4.9e-20; tive 54; Mismatches 137; Indels
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Copyright (c) 1993 - 2000 Compugen Ltd
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CLT1_PIG
AG2R_PIG
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AG2R_CANF
AG2R_RABIT
AG2R_CAVPO
P2Y9_HUMAN
AGP68_HUMAN
AGP68_HUMAN
AG2R_RAT
AG2R_MOUSE
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O14626 homo sapien
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5 homo sapien
6 cavia porce
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3 sus scrofa
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KIO1_HUMAN
ID KIO1_HUMAN
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
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CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC...) (POTENTIAL).
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Pred. No. 3.4e-45;
0; Mismatches 105
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Sciurognathi; Muridae;
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Best Local Similarity
Matches 132; Conser
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Probable G p
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MEDLINE-98036061; pubMed=9370294;

Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M., Duckett M., Colden-Fleet M., Kelleher K., Kriz R., LaVallie E.R., Spaulding V., Stover J., Williamson M.J., McCoy J.M.;

"A genetic selection for isolating cDNAs encoding secrete 198:289-296(1997).

"In Transport M. T. Collins Collins of the Collins of 
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Metazoa; Primates; C
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Pred. No. 5.le
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  a collaboration
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Q9RIK6;
16-OCT-2001
16-OCT-2001
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Probable G p
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DOMAIN
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PROSITE; PS500237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

EXTRACELLULAR (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
 Eukaryota; Metazoa;
Mammalia; Eutheria;
                       Mus musculus (Mouse)
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1 (Rel. 40, Last sequence up
1 (Rel. 40, Last annotation
protein-coupled receptor GP
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Chordata;
Rodentia;
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .)
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Pred. No. 3
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6 (POTENTIAL
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 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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on update)
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Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99326137; PubMed-10395919; Schoneberg T., Schulz A., Grosse R., Schultz G., Gudermann T.;
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                                                                                                                                         QASQNFSGVPNVTS-CPMDEKLLSTVLTTFYSVIFLVGLVGNIIALYVFLGIHRKRNSIQ 83
RHNAKGEAIFNFVLVVMFWLIFLLIILSYIKIGKNLLRISKRRSKFPNSGKYATTARN--
            EFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYR-SYVRTR--GVGKVPRKKVNVK 237
                                                                                                                                                                                        101;
                                                                   DRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKS 180
                                                                                                      IFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITI 120
                                                                                          IYLLNVAVADLLLIFCLPFRIMYHINQNKWTLGVILCKVVGTLFYMNMYISIILLGFISL
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2 (POTENTTAT
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Pred. No. 4.8e-21;
2; Mismatches 154;
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N-LINKED
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EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL)
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CYTOPLASMIC (
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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4 (POTENTIA
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7 (POTENTIAL).
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-LINKED (GLCNAC. ..) (POTENTIAL).
-LINKED (GLCNAC. ..) (POTENTIAL).
-LINKED (GLCNAC. ..) (POTENTIAL).
-LINKED (GLCNAC. ..) (POTENTIAL).
-LINKED (GLCNAC. ..) (POTENTIAL).
C04E1C1A52521045 CRC64;
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RESULT
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GPRY_HUMAN STANDARD; PR

O9UPC5; O95853;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last seque

01-MAR-2002 (Rel. 41, Last annot
            EMBL; AF039686;
EMBL; AF118670;
EMBL; AK027780;
MIM; 300241;
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or send a
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Schultz G., Gudermann T.;
*A novel subgroup of class I G-protein-coupled
*Blochim. Biophys. Acta 1446:57-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                   "Physical mapping and exclusion of GPR34 as the congenital stationary night blindness type 1."; hum. Genet. 107:89-91(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20434921; PubMed=10982042; MEDLINE=20434921; PubMed=10982042; MEDLINE=20434921; Propriet M., Pesch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-Fetal brain;
TISSUB-Fetal brain;
MEDLINE-99326137; PubMed=10395919;
MEDLINE-99326137; Schulz A., Grosse R.,
                                                                                                                                                                                                                                                      submitted (MAY-2001) to the EN-
-!- FUNCTION: ORPHAN RECEPTOR.
                                                                                                                                                                                                                                                                 Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi Pujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jacobi F.K., Broghammer M.,
Meindl A., Pusch C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marchese A., Sawzdargo M., Nguyen T., Cheng R., Heng H.H., Nowal III D.-S., Lynch K.R., George S.R., O'Dowd B.F.; "Discovery of three novel orphan G-protein-coupled receptors."; Genomics 56:12-21(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-99156852; PubMed=10036181;
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European Bioinformatics Institute. The
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Receptor; G-protein coupled receptor; Tran
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16-OCT-2001 (Rel. 40, Last annotation
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Chase P.B., Halonen M., Regan J.W.;

"Cloning of a human platelet-activating factor receptor gene:
evidence for an intron in the 5'-untranslated region.";
Am. J. Respir Cell Mol. Biol. 8:240-244(1993).

-! FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM.

-!- SUBCELULLAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-92347886; PubMed-1322356;

Seyfried C.E., Schweickart V.L., Godiska R., Gray P.W.;

"The human platelet-activating factor receptor gene (PT no introns and maps to chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Leukocyte;

MEDLINE=92041873; PubMed=1657923;

Nakamura M., Honda Z., Izumi T., Sakanaka C., Mutoh H., Minami I

Bito H., Seyama Y., Matsumoto T., Noma M., Shimizu T.;

"Molecular cloning and expression of platelet-activating factor receptor from human leukocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Behal R.H., Debuysere Submitted (XXX-1992) t
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MEDLINE-93112021; PubMed-1281995;
Sugimoto T., Tsuchimochi H., McGr
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J. Biol. Chem. 2
                                                                                                              use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-93192035; PubMed-8383507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and characterization of the platelet-activating factor receptor gene expressed in the human heart."; Biochem. Biophys. Res. Commun. 189:617-624(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ye R.D., Prossnitz E.R., Zou A., Cochrane C.G.; "Characterization of a human CONA that encodes a for platelet activating factor."; Biochem. Biophys. Res. Commun. 180:105-111(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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L07334;
S56396;
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AAA60001.1;
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BAAA601050.1;
AAAA60214.1;
AAAA60214.1;
AAB24695.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00001;
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                               VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                      DOMAIN
              240
                              177
                                                               121
                                                                               128
236
                                               180
                                                                                               61
                                                                                                               68
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                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JH0479;
A40191;
A41079;
                                                                                                                                              PGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIR--SKSNFI-IFLKNTV
TVLAVFIICFVPHHVVQLPWTLAEL-GFQDSKFHQAINDAHQVTLCLLSTNCVLDPVIYC
                             YEKGSVPVLIIHIFIVESFELVELIILFCNLVIIRTLLMQPVQQQRNAEVKRALMM-VC
                                      SEFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVF
                                                                                               MADMLFLITLPLWIVYYQNQGNWILPKFLCNVAGCLFFINTYCSVAFLGVITYNRFQAVT
                                                                                                       ISDLLMILTFPEKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTT::|:| ::| | |::||:| | |::|
                                                                                                                              IIIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYF
                                                             RPIKTAQANTRKRGISLSLVIWVAIVGAASYFLILDS---
                                                                             RPFKTSNPKNLLGAKILSVVIW-----AFMFLLSLPNMILTNRQPRDK----NVKKCSFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCR_0414;
GCR_0478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCR_0260;
GCR_0285;
                                                                                                                                                                107; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR01153; PAFRECEPTOR.; PS00237; G_PROTEIN_F
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000276; GPCR_Rhodpsn
0001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    coupled
                                                                                                                                                                                                       316
342
                                                                                                                                                                                                                                                                                              JH0479.
A40191.
A41079.
                                                                                                                                                                Conservative
                                                                                                                                                                                                                      28
95
227
227
227
                                                                                                                                                                                                                                                                                338
                                                                                                                                                                                                        AA;
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66
95
228
228
247
316
316
                                                                                                                                                                                                                                                                                                                                                                                                                                                    G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                     16
38
54
91
                                                                                                                                                                       22.2%;
32.6%;
                                                                                                                                                                                                        ₹.
                                                                                                                                                                61;
                                                                                                                                                                                                               KR -> TG (IN REF. 4).
KR -> TT (IN REF. 6).
P -> A (IN REF. 6).
K -> N (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                      3 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                               /FTId=VAR_011851.
N -> S (IN DBSNP:
                                                                                                                                                                                                                                                                                                                      7 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC
                                                                                                                                                                       Score 394;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                      6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                         890073C9EBA79228
                                                                                                                                                                                                                                                                -> P (IN
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                                                                                                                                                                                                                                                                                                               SIMILARITY
                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                               > P (IN REF. 6).
> L (IN REF. 6).
> R (IN REF. 6).
                                                                                                                                                                                                                                                                               S (IN DBSNP:5939).
                                                                                                                                                                       DB 1;
.6e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                TNTVPDSAGSGNVTRC-FEH
                                                                                                                                                                                                          CRC64;
                                                                                                                                                                              Length
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                26;
                                                                                                                                                                Gaps
                                                                                                                                 60
                                                                176
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                               235
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β 8 8

FLCKSFRN-----SLISMLKCPNSAT

320 322

300 295

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RESULT
                                                                                    TRANSMEM
DOMAIN
            CARBOHYD
DISULFID
                                            TRANSMEM
DOMAIN
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01-AUG-1991
01-OCT-1996
                                                                                                                                                                                                           PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _CAVPO
                                                                                                                                                                                                                                                                                       EMBL; X56736; CAA40060.1; PIR; S13638; S13638.
                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          use by non-profit institumodified and this statement
                                  CARBOHYD
                                                                DOMAIN
                                                                           TRANSMEM
                                                                                                          DOMAIN
                                                                                                                   TRANSMEM
                                                                                                                               DOMAIN
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                                                                                                                                                                       DOMAIN
                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                     Chemotaxis.
                                                                                                                                                                                                                                               PRINTS; PR01153; PAFRECEPTOR.
                                                                                                                                                                                                                                                          Pfam; PF00001;
                                                                                                                                                                                                                                                                             GCRDb; GCR_0034;
                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T Okado H., Toh H., Ito K., Miyamoto T., Shimizu T.; "Cloning by functional expression of platelet-activating receptor from guinea-pig lung."; Nature 349:342-346(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19
01-OCT-1996 (Rel. 34
Platelet activating
                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P21556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAFR_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91101726; PubMed=1846231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-MUSCLE COUNTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLTKKFRKHLTEKFYSMRSSRKCSRATT
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169
90
342
                                          AA;
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. 19, Last
. 34, Last
ing factor
                                           ormatics Institute. There are no resinstitutions as long as its content
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 MW;
       7 (POTENTIAL).
CYTOPLASMIC (P
CYTOPLASMIC (GLCN
N-LINKED (GLCN
N-LINKED (GLCN
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                           is not removed
                                                                         CYTOPLASMIC
6 (POTENTIAL
                                                                                                                   CYTOPLASMIC
4 (POTENTIAL
                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                      EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                                                                                              EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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Hystricognathi; Caviidae;
                                                                         (POTENTIAL)
                                                                                                                   (POTENTIAL)
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 B6413B3A5C87B175
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                  (GLCNAC. .
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                                       (POTENTIAL).
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 CRC64
                   (POTENTIAL)
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                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                              restrictions
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Best Local S
Matches 103
InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                   GCRDb;
                                                               EMBL; L08177; PIR; B45680; E
                                                                                                   entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                      the
                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                       MIM; 605741;
                                                                                                                              modified
                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                               "Epstein-Barr virus-induced genes: f protein-coupled peptide receptors.";
J. Virol. 67:2209-2220(1993).
                                                                                                                                                                                                                                                                                                                                   Birkenbach M.P.,
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P32249;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                          Kieff E.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=93188173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EBV-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EBI2_HUMAN
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                                                                                                                                                                                          TISSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES.
INDUCTION: BY EBV.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Expurpean Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                         FUNCTION: ORPHAN RECEPTOR. PROBABLE MEDIATOR (
LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS
TISSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHLSEKLNIMRSSQKCSRVTTDTGTEMAIPINHTPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ICIVLGFFIVFLLILECNLVIIHTLLRQPVKQQRNAEV-RRRALWMVCTVLAVFV
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                                                   GCR_0499;
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                                                                                                                             non-profit instituend this statement
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(Rel. 27, Last sequence update)
(Rel. 40, Last annotation updat
G protein-coupled receptor 2 (E
                                                              B45680.
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                                                                                                                                                                                                                                                                                                                                     Josefsen
                                                                                                                                                                                                                                                                                                                                 PubMed=8383238;
Josefsen K., Yalamanchili R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
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Pred. No. 8.3e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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There are no res
ng as its content
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RESULT
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Best Local S
Matches 94
                                                                   01 MAR-2002 (Rel. 41, Created)
01 MAR-2002 (Rel. 41, Last sequence update)
01 MAR-2002 (Rel. 41, Last annotation updat
01 MAR-2002 (Rel. 41, Last annotation updat
Cysteinyl leukotriene receptor 2 (CysLTR2).
CYSLTR2 OR CYSLT2.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Cranlata; Ver
Mammalla; Eutheria; Cetartiodactyla; Suina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
 Kamohara M.,
Ohishi T., So
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                                                                                                                                                                                                             CLT2_PIG
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DOMAIN
                              SEQUENCE FROM N.A.
                                                          NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                           FTVCLMNFNCCMDPFIYFFACKGYKRKVMRMLK-RQVSVSISSAVKSAPEENSREMTETQ 350
                                                                                                                                                                                                                                                                                                                                                                    STLWLTSLNACLDFFIYFFLCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SISFLGLITIDRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMI--LTNRQPR 168
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                                                                                                                                                                                                                                                                                                                                                                                                    SGVNK---KALNT-IILIIVVFVLCFTPYHVAIIQHMIKKLRFSNFLECSQRHSFQISLH
                                                                                                                                                                                                                                                                                                                                                                                                                                  RGVGKVPRKKVNVKVFIIIAVFFICFVPFHFARIPYTLSQTR--DVFDCTAENTLFYVKE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RITCMEYPNFEETKSLPW--ILLGACFIGYVLPLIILICYSQICCKLFRTAKQNPLTEK
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PS50262;
n coupled
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                                                                                                                                                                                                           STANDARD;
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G_PROTEIN_RECEP_F1_2; 1.
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                                                                        Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
ki J., Matsumoto M., Matsumoto
Matsushime H., Furuichi K.;
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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Sus.
                Saito
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

-i-FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol. calcium second messenger system (By similarity).

-i- SUBCELLULAR LOCATION: Integral membrane protein.

-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as permodified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rnterPro; IPR000276;
Pfam; PF00001; 7tm_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB052662; BAB60817.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of the cloned rat and porcine cysteinyl leukotriene receptors.";
                                                                                                                                                         CLELNSN-KYTKLKTMNYVALVVGFVLPFGTLSICYLLIIRALLKVEVPESGL-RLSHRK
                                                                                                                                                                              CSFLKSEFGLVWHEIVNYICQVI-FWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKK
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NPFLYYFAGENFKDRLKSALR
                                                                              ALITVIIALIIFLLCFLPYHVLRTLHLLEWKAD----KCKDRLHKAVAVTLALAAANSCF
                                                                                                                                                                                                                                                                                                                                                                                                   MEPNSTLGNHNSNRSCTTENEK--REFYPIVYLVIFIWGALGNGFSIYVFLKPYKKSTSV
                                   DPFIYFFLCKSFRNSLISMLK
                                                                                                                    VNVKVFIIIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACL
                                                                                                                                                                                                                                        LTVLSVVRFLATVHPFRLLHTTSIKNAWILCGVIW--IFIMASSTVLLKNGSEQKDNVTL
                                                                                                                                                                                                                                                                             LGLITIDRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKK 174
                                                                                                                                                                                                                                                                                                                    NVFMLNLAISDLLFTITLPFRVDYYLRGSNXIFGDTP-----CRIMSYSMYVNMYSSIYF
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Pred. No. 4.3e-18;
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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N-LINKED (GLC
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CYTOPLASMIC (
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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PAFR_MOUSE
Query Match
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Q62035;
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor.send.an.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A murine platelet-activating factor receptor gene: cloning, chromosomal localization and up-regulation of expression by lipopolysaccharide in peritoneal resident macrophages."; Biochem. J. 314:671-678(1996).

-i- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTAC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMO MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129/SV;
MEDLINE=96239129; PubMed=8670084;
Martenda Y., Nakamura M.,
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCRDb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                     G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1153; PAFRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D50872; BAA09468.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noma M., Shimizu T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platelet activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTION VIA A GENERAL ACTION HESCENDER SYSTEM.
CALCIUM SECOND MESSENGER SYSTEM.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:106066; Ptafr.
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(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
tivating factor receptor (PAF-R).
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                                                             Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein;
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N-LINKED (GLCNAC. . .) (
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6 (POTENTIAL
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5 (POTENTIAL).
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7 (POTENTIAL).
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                                                CAA8CDDBD8D26897 CRC64;
                                                                                                                                                            (POTENTIAL)
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366;
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   PRINTS; PR01153; PAFRECEPTOR PROSITE; PS00237; G_PROTEIN_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAFR_RAT
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G_PROTEIN_RECEP_F1_1;

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Best Local Similarity Matches 96; Conserv
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-oct-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the statement of the statement of the swiss of the statement of t
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Spleen;
MEDLINE-94222063; PubMed-8168510;
MEDLINE-942206510;
MEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                          GCRDb; GCR_0985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               platelet-activating-factor-receptor cDNA.";
Eur. J. Biochem. 221:211-218(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bito H., Honda 2., Nakamura M., Shimizu T.; "Cloning, expression and tissue distribution
Pfam; PF00001; 7tm_1;
                                                                                                                                                                               EMBL; U04740; AAA18422.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                        [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMALL INTESTINE, KIDNEY, LUNG, LIVER AND BRAIN. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: PRESENT IN ALMOST ALL ORGANS INCLUDING
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                                                  IPR000276; GPCR_Rhodpsn.
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4; Mismatches 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą
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PROSITE; PS50262;

G_PROTEIN_RECEP_F1_2; 1.

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Best Local Similarity
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                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
P2Y purinoceptor 5 (P2Y5) (Purinergic receptor P2RY5.
                                                                                                                                                                                         CHICK
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DOMAIN
MEDLINE-93329058; PubMed-8393036; Kaplan M.H., Smith D.I., Sundick R.S. "Identification of a G protein couple
                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                SEQUENCE FROM N.A. TISSUE=T-cell;
                                                             NCBI_TaxID=9031;
                                                                                 Archosauria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYKITQVLFPLLYTVLFFVGLITNGLAMRIF---FQIRSKSNFIIFLKNTVISDLLMILT 76
                                                                                                                                                                                                                                                   IYFFLCKSFRN-----SLISMLKCPNSATS
                                                                                                                                                                                                                                                                                   KVFIIIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPF 296
                                                                                                                                                                                                                                                                                                                FITSCFFLVFF-----LIFYCNMVII---HTLLTRP-----VRQQRKPEVKRRALWM
                                                                                                                                                                                                                                                                                                                                     FLKSEFGLVWHEIVNYICOVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNV 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DSEFRYTLFPIVYSVIFVLGVVANGYVLWVFATLYPSKKLNEIKIFMVNLTVADLLFLMT
                                                                                                                                                                                                                                                                        -VCTVLAVFVICFVPHHVVQLPWTLAELG--YQTNFHQAINDAHQITLCLLSTNCVLDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 362; DB 1; 1
Pred. No. 9.1e-18;
6; Mismatches 120;
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N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

BY SIMILARITY,

DOAF7290C3D34A5B CRC64;
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).
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6 (POTENTIAL
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2 (POTENTIAL
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EXTRACELLULAR (POTENTIAL)
                                                                                Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
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Best Local Similarity
Matches 87; Conser
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DISULFID
SEQUENCE
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DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T cells.";
J. Immunol. 151:628-636(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01067; P2Y5PRNOCPTR PRINTS; PR01157; P2PURNOCEPTR
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Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral TISSUE SPECIFICITY: INDUCED IN
                                                                                                                                            FVPYNITLILYSLMRTQTWINCSVVTAVRTMYPV---TLCIAVSNCCFDPIVYYF
                   FVPFHFARIPYTLSQTRDVFDC---TAENTLFYVKESTLWLTSLNACLDPFIYFF
                                                                                                        SNPKNLLGAKILSVVIWAFMFLLSLPNMIL -- TNRQPRDKNVKKC -- SFLKSEFGLVWHE
                                                                                                                              FVFTLPFRIYYFV-VRNWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS
                                                                                                                                                                         SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLL
                                         IVIFIEIVGFFIPLILNVTCSTMVLRTLNKPLTLSR--NKLSKKKVLKMIFVHLVIFCFC
                                                              IVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFIC
                                                                                    KTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQ-NNTEQRTCFENFPESTWKTYLSR
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                                                                                                                                                                                                                              Score
Pred.
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5 (POTENTIAL)
                                                                                                                                                                                                                                                                          POTENTIAL. 4214E969633B6F7D CRC64;
                                                                                                                                                                                                                                                                                                          7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .)
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC
2 (POTENTIA)
                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL).
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IN ACTIVATED T-CELLS
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                               357.5;
No. 1.7
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                                                                                                                                                                                                                               DB 1;
L.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                      125;
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                                                                                                                                                                                                                                         Length
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                                                                                    180
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RESULT 13 CLT2_HUMAN

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CLT2_HUMAN STANDARD; PRT; 346 AA.

QNS75; Q9HCQ2;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 2 (CysLTR2) (PSEC0146) (HG57) (HPN321).
CYSLTR2 OR CYSLT2 OR CYSLT2R.
                                                                                                    entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombé Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.N., Lynch K.R., Evans J.F.; "Characterization of the human cysteinyl leukotriene 2 receptor."; Biol. Chem. 275:30531-30536(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                             use by non-profit modified and this st
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way made that the state of the state 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20374466; PubMed=10913337;
Takasaki J., Kamohara M., Matsumoto M.,
Nishikawa T., Kawai Y., Masuho Y., Isog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and characterization of a leukotriene receptor: discovery of a subtype Mol. Pharmacol. 58:1601-1608(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The molecular characterization and tissue distribution cysteinyl leukotriene CysLT2 receptor.";
Biochem. Biophys. Res. Commun. 274:316-322(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suga H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2001) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11093801;
Nothacker H.-P., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Homo sapiens cysteinyl leukotriene receptor 1 like receptor."; submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. Ite response is mediated via a G-protein that activates a phosphatidylinositol-
                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed, with highest levels in the heart, placenta, spleen, peripheral blood leukocytes and adrenal gland. In lung, expressed in the interstitial macrophages, and slightly in smooth muscle cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                             pulmonary vascular endothelium. The rank
the leukotrienes is LTC4 = LTD4 >> LTE4.
SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calcium second messenger system. Stimulation by BAY 19773, a partial agonist, induces specific contractions of pulmonary veins and might also have an indirect role in the relaxation of the
                                                AB038269;
                        AF254664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R., S.D.L. Jr., Zeng Z., Liu Q., Ma.L., Clements M.K., Coulom Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
                                                                                                    d and this statement is not removed a requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-346
BAB03601.1; -. AAG17281.1; -. AAK69485.1; -.
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Primates;
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                                                                                                                               agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to M., Saito
, Isogai T.,
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selective agonist.";
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Suzuki, Y., Su
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01-NOV-1997
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EMBL; AB041644; BAB16379
MIM; 605666; -
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InterPro; IPR000276; GPCR_Rhodpsn.
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 (African clawed
                                                                                                                          STANDARD
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42
63
72
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G_PROTEIN_RECEP_F1_2;
                                             35, Created)
35, Last sequence up
39, Last annotation
                                    (P2Y8)
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY
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N-LINKED (GLCNAC...) (
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N-LINKED (GLCNAC...) (
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Pred.
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7 (POTENTIAL).
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No. 8.6
                                                                       update)
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9.6e-17;
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(POTENTIAL).
(POTENTIAL).
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Best Local Similarity
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SEQUENCE
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DISULFID
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Of Xenopus embryos:";

J. Biol. Chem. 272:12583-12590(1997).

J. Biol. Chem. 272:12583-12590(1997).

FUNCTION: RECEPTOR FOR EXTRACELLULAR ATP, UTP, CTP, GTP AND ITP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. MAY PLAY A KEY ROLE IN THE EARLY DEVELOPMENT OF NEURAL TISSUE.

-I- SUBCELLULAR LOCATION: Integral membrane protein.

-I- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50252; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCRDb; GCR_1419; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X99953; CAA68213.1; -. HSSP; P34996; 1DDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bogdanov Y.D., Dale L., King B.F., Whittock N., "Early expression of a novel nucleotide recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Neural plate; MEDLINE-97284734; PubMed-9139711;
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                                                                                                   79
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                                                                                                                                                                                                21
                                               IDRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLK
                                                                                                                                                                                                                                        MQAVDNLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFF-QIRSKSNF
VHRYRGVCHPITSLRRMNAKHAYVICALVWLSVTLCLVPNLIFVTVSPKVKNTICHDTTR
                                                                                              TVYMFNLALSDTLYVLSLPTLVYYYADKNNWPFGEVLCKLVRFLFYANLYSSILFLTCIS
                                                                                                                                           IIFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLIT 119
                                                                                                                                                                                             MKLLMNLTN--DTEDICVFDEGFKFLLLPVSYSAVFMVGLPLNIAAMWIFIAKMRPWNPT 78
                                                                                                                                                                                                                                                                                               93;
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1 49 EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                            Conservative
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29.3%;
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                                                                                                                                                                                                                                                                                            60;
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BY SIMILARITY.
N-LINKED (GLCN
N-LINKED (GLCN
                                                                                                                                                                                                                                                                                       Score 347.5; DB 1;
Pred. No. 1.3e-16;
0; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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-LINKED (GLCNAC. . .) (POTENTIAL).
B2CF24812F3C19F2 CRC64;
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                DOMAIN
TRANSMEM
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TRANSMEM
                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic cloning, alternative splicing,
characterization.";
J. Biol. Chem. 276:47489-47495(2001).
  DOMAIN
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                                                                      TRANSMEM
                                                                                     DOMAIN
                                                                                                  TRANSMEM
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                                                                                                                                                                       G-protein
DOMAIN
                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1131, Austral H., Figueroa D.J., Austral Hui Y., Yang G., Galczenski H., Figueroa D.J., Austral Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.; Copeland N.G., Gilbert b.J., Jenkins N.A., Funk C.D.; The murine cysteinyl leukotriene 2 (CysLT2) receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cysteinyl leukotriene receptor CYSLTR2 OR CYSLT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q920A1;
01-MAR-2002
                                                                                                                 DOMAIN
                                                                                                                                                                                                                              Pfam; PF00001;
                                                                                                                                                                                                                                                        EMBL; AF331658; AAK97354.1;
                                                                                                                                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
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PubMed=11591709;
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                                                                                                                                                                                                                                         InterPro; IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed at low levels, with highest expression in the spleen, thymus and adrenal gland, and lower in the kidney, brain and peripheral blood leukocytes.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Siol. Chem. 276:47489-47495(2001).

FUNCTION: Receptor for cysteinyl leukotrienes. The response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mediated via a G-protein that activates a phosphatidylinositol-
calcium second messenger system. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTD4.
                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                               00001; 7tm_1; 1.

PS00237; G_PROTEIN_RECEP_F1_1;

PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                  coupled
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 receptor;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                   Transmembrane; Glycoprotein EXTRACELLULAR (POTENTIAL).
                                                                                                                             CYTOPLASMIC
2 (POTENTIAL
                                                                                               2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL)
             CYTOPLASMIC
6 (POTENTIAL
                                         EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
                                                                     CYTOPLASMIC 4 (POTENTIA)
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
              (POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309
                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                              FALSE_NEG
                                                                                  (POTENTIAL).
                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                            Usage
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Best Local Similarity 27.6%;
Matches 88; Conservative 6
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DOMAIN
DISULFID
CARBOHYD
SEQUENCE
                                                                                                 111 YFLTVLSVVRFQATVHPFRMFHVTSVRSAWILCGIIW--VFIMASSALLLVNGQEEKDNI 168
291 ACLDPFIYFFLCKSFRNSL 309
:|:||:|:|:|:|
282 SCFNPFLYYFAGENFKARL 300
                                                                                                                                                                 113 SFLGLITIDRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNV 142
                                                  227 RKALTT-IVIAMITELLCELPYHALRTLHLVTWDKD----SCGDVLHKATVITLTMAAAN 281
                                                              231 RKKVNVKVFIIIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLN 290
                                                                                                                                                                                                    61 MLNLATSDELEISTLPERADYYERGSNWIEGD------LACRYMSYSLYVNMYTSI 110
                                                                                                                                                                                                                    272
293
95
14
309 AA;
                                                                                                                                                                                                                                                                                                                                                                     292 7 (POTENTIAL).
309 CYTOPLASMIC (POTENTIAL).
171 BY SIMILARITY.
14 N-LINKED (GLCNAC. . .) (POTENTIAL).
35227 MW; 327B14A6EDDD2A02 CRC64;
                                                                                                                                                                                                                                                                                                        8; Score 344; DB 1; Length 309;8; Pred. No. 1.3e-16;68; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                         Indels 34; Gaps
                                                                                                                                                                                                                                                                                                          10;
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Search completed: September 6, 2002, 15:34:40 Job time: 238 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
1748
1528.5
1528.5
1528.6
829
741.7
741.7
699.5
699.5
685.5
553.5
553.5
388.5
                                                                                                                                                                                                    Score
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1: sp_archea:*
2: sp_bacteria
 100.0
98.3
98.5
87.5
86.0
46.6
44.7
39.1
39.1
31.4
25.2
21.9
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Match Length
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Gapop 10.0 , Gapext 0.5
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1778
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sp_rodent:*
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sp_rvirus:*
sp_bacteriap:*
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 342
343
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            Q9H244
Q9BGT4
Q95KC3
Q95CV9
Q9EPV4
Q9EPX4
Q9BV21
Q9BSG6
Q9BY21
                                                                                                                                                                                                      IJ
  Q9GK76
                                                                                                                                                                                                                                        SUMMARIES
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Q9be53 macaca fasc
Q9bxc2 homo sapien
Q9by61 homo sapien
Q9tty5 bos taurus
Q9gk76 capra hircu
                                                       Q9h244 homo sapien
Q9bgt8 macaca fasc
Q95kc3 macaca fasc
Q9cpv9 mus musculu
Q9cpv4 rattus norv
Q9bpv8 homo sapien
Q9d812 mus musculu
Q9esg6 mus musculu
Q9esg6 mus musculu
Q9esg6 homo sapien
Q9by21 homo sapien
Q9by71 mus musculu
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ALIGNMENTS

ate) RECEPTOR RECEPTOR A: Englan A: Juli rgeted b rgeted b rein-cou	H244 Q9H244 Q9H244; Q9H244; Q9H244; Q9H244; Q1-MAR-2001 (TrEMBLrel. 16, Cr Q1-MAR-2001 (TrEMBLrel. 19, La Q1-DEC-2001 (TrEMBLrel. 19, La P2Y12 PLATELET ADP RECEPTOR (G (GI-COUPLED ADP RECEPTOR HORK3 HOMO Sapiens (Human)
pdate) update) update) update) update; indical palend L., cominidae; Homo. i. G., England L., den A., Julius D.J., r Targeted by J., Smith M., Qiao X., Palmer K., Bayne M., protein-coupled receptor K.; receptor:; receptor, the P2Y1	pdate) update) LED RECEPTOR SP1999)

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Best Local S
Matches 342
                                           TISSUE-FRONTAL LOBE LEFT;
Osada N., Hida M., Kusuda J., Tanuma R., Is
Osada N., Hida M., Kusuda J., Tanuma R., Is
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from
libraries.";
Submitted (FEB-2001) to the EMBL/GenBank/DE
EMBL; AB056385; BAB33041.1; -.
InterPro; IPR000276; GPCRRhODOPSN.
PRINTS; PR000217; GPCRRHODOPSN.
PROSITE; PR550262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         99BGT8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 39.5 KDA PROTEIN.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor.";
Mol. Pharmacol. 60:432-439(2001).
EMBL; AF313449; AAG48944.1; -.
EMBL; AF321815; AAK00948.1; -.
EMBL; AB052684; BAB60824.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODDDSN.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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     Hypothetical protein. SEQUENCE 342 AA; 39497
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae;
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Query Match

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Best Local
Matches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-MEDULLA OBLOGATA;
Osada N., Hida M., Kusuda J., Tanuma F
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca fascicularis (Crab eating macaque) (Cynomolgus monk
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammallia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q95KC3 PRELIMINARY; PRT; 342 AA.
Q95KC3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 39.5 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2001) to the EMBL; AB062981; BAB60747.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 342 AA; 3
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  181
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3; Mismatches
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3; Mismatches
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ertebrata; Euteleostomi;
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RC STRAIN=CS7BL/GG; TISSUE=TESTIS, AND HIPPOCAMPUS;

RX MEDLINE=21085660; PubMed=11217851;

RA ARAMAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackeabush J.,

RA Schriml L.M., Stabbli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Bustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.,

PEMBL; AKOl1809; PA192561 1; -

DR MGD, MGI:192038; 290079B22Rik.

DR MGD, MGI:192038; 290079B22Rik.

DR MGD, MGI:192037; GepcRRHODOPSN.

DR PANTS; PR00237; GepcRRHODOPSN.

SQ SEQUENCE 347 AA; 39473 MW; F107488E57E025F1 CRC64;
                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 299
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01-JUN-2001 (TIEMBLIEL 17, Last sequence update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation update)
4921504D23RIK PROTEIN (2900079B22RIK PROTEIN).
PRY12 OR 4921504D23RIK OR 2900079B22RIK.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
        132
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                                                                                                                                                                                                                                         87.5%; Score 1555.5; DB 11; Length 347; 88.7%; Pred. No. 2.7e-131; tive 16; Mismatches 21; Indels 1;
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Query Match 86.0
Best Local Similarity 86.9
Matches 293; Conservative
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Nature 409:202-207(2001).
EMBL; AF313450; AAG48945.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; Tym_1; Tym_1; Tym_1; Tym_1; Tym_2; Tym_
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Q9EPX4;
01-MAR-2001 (TrEMBLrel. 16, C:
01-MAR-2001 (TrEMBLrel. 17, L:
01-JUN-2001 (TrEMBLrel. 17, L:
P2Y12 PLATELET ADP RECEPTOR.
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STRAIN-SPRAGUE-DAWLEY;
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-21037966; PubMed-11196645;
MEDLINE-21037966; PubMed-111966645;
MEDLINE-21037966; PubMed-111966645;
MEDLINE-21037966; PubMed-111966645;
MEDLINE-21037966; PubMed-111966645;
MEDLINE-210379666; PubMed-111966645;
MEDLINE-210379666; PubMed-111966645;
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MEDLINE-2103796666; PubMed-111966666; PubMed-1119666666; PubMed-1119666666; PubMed-1119666666; PubMed-111966666; PubMed-111966666; PubMed-11196666; PubMed-111966666; PubMed-111966
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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RNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM
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TTRPEKTSSPSNLLGAKILSVAIWAEMFLLSLPNMILTNRRPKDKDITKCSFLKSEEGLV
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86.9%;
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Pred. No. 6.9e
17; Mismatches
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.es 22;
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Best Local S
Matches 155
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"IdentLification of a Novel Human ADP Rec J. Biol. Chem. 276:41479-41485(2001).
EMBL; AF345565; AAK29068.1; --
EMBL; AF295368; AAK01864.1; --
EMBL; AF411113; AAL26484.1; --
EMBL; AF406692; AAL01038.1; --
InterPro; IPR000276; GPCR_Rhodpsn.
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Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKSG77 (G-PROTEIN COUPLED RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDILINE-21172992; PubMed-11273702;

Wittenberger T. Schaller H.C., Hellebrand S.;

"An expressed sequence tag (est) data mining stra
the discovery of new 9-protein coupled receptors.

J. Mol. Biol. 307:799-813(2001).
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GPR86).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of FKSG77, a novel gene encoding a putative protein-coupled receptor."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21458557; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., V
Lewis T., Evans J.F., George S.R., O'Dowd B.
"Discovery and mapping of ten novel G protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-HEART;
Wang Y., Gong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKSG77 OR GPR86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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135
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KPVFAKTVSIFIWFFLFFISLPNMILSNKEATPSSVKKCASLKGPLGLKWHQMVNNICQF
                                           NLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEIVNYICQV 196
                                                                                            LPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRNIFLK
                                                                                                                         FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
                                                                                                                                                                                                 CPRDTRIVQLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIIYLKNTLVADLIMTLM 74
                                                                                                                                                                                                                                            CTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLLMILT 76
                                                                                                                                                                                                                                                                                                                          Similarity
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etazoa; Chordata;
theria; Primates;
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                                                                                                                                                                                                                                                                                                                       46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                         38440 MW;
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                                                                                                                                                                                                                                                                                                                          Score 829; DB 4;
Pred. No. 2.4e-66;
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                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vanti W.B., B.F.;
                                                                                                                                                                                                                                                                                                   102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coupled
                                                                                                                                                                                                                                                                                                                                              Length 333;
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizki Y.;
                                                                                                                                Query Match
Best Local S
Matches 151
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Q9D812;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
2010001L06RIK PROTEIN.
                                                                                                                                                                                                                   PRINTS; PRO0237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RE
PROSITE; PS50262; G_PROTEIN_RE
SEQUENCE 337 AA; 38693 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; MEDLINE=21085660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).

Mus musculus (Mouse).

Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
"Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawai J., Shinagawa A., Shibata K., Yoshino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                      InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                         MGD; MGI:1921441; Gpr86
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KNTLVADLIMALMLPFKILSDSHLAPWQLRGFVCTLSSVVFYETMYVGIMMLGLIAFDRF
                             KNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFWTVFILMLVFYVVIAKKVYDSYRKSKSKDRKNNKKLEGKVFVVVAVFFVCFAPFHFAR
                                                                 NTTGMQGFNKSERCPRDTRMTQLLFPVLYTVVFLAGILLNTVALWVFVHIPSNSTFIVYL
                                                                                                                                   151;
                                                                                                                                                                                                                                                                                                                                       AK008013; BAB25409.1;
                                                                                                                                                   Similarity
                                                                                                                                                                                                                    PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
337 AA; 38693 MW; 2C1A76FBF893D5EA CRC64;
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6J; TISSUE=SMALL INTESTINE;
660; PubMed=11217851;
7, hara K., Yosh
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                                                                                                                                     Mismatches
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
7 TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF17721; AAG09275.1; . InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "7 transmembrane G progenitors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Lee B.C., Scadden
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                                                                                                                                        VFFICEVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCK 303
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338 AA; 38861 MW; 4376B50622A68A4E CRC64;
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01-JUN-2001 (TrEMBLrel. 17
01-DEC-2001 (TrEMBLrel. 19
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GPR87 OR GPR95.
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Q9BY21;
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                                             Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
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G PROTEIN-COUPLED RECEPTOR.
  SEQUENCE FROM N.A
                                                                                                                            Homo sapiens (Human).
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TISSUE-PLACENTA;
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Metazoa; Chordata; C
Metazoa; Primates; (
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(TIEMBLrel. 19, Last sequence update)
(TIEMBLrel. 19, Last annotation update)
78 FIS, CLONE PLACE1003238, WEAKLY SIMILAR TO PROBABLE
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19, Last annotation updat
D RECEPTOR 87.
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Pred. No. 9.6e-55;
7; Mismatches 113;
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                                                                          Craniata; Vertebrata; Catarrhini; Hominidae
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-i- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMIC -i- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEDED: -i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEMBL; AF431114; AAC126485.1; -.

R EMBL; AF431114; AAL26485.1; -.

R INTERPRO; IPRO00276; GPCR_Rhodpsn.

Ffam: PF00001; Tum_1; 1.

R PROSITE; PR00237; GPCRRHODDPSN.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Transmem G-protein coupled receptor; GFS0295BE5D10F CRC64;
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SEQUENCE FROM N.A. MEDLINE=21172992; P Wittenberger T., Sc "An expressed seque
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[2]
SEQUENCE FROM N.A.
MEDLINE=21458557; P
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Gene 27!
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                  GPR87
                                                                                                                                                                                                                                                                                                                                    G-PROTEIN COUPLED
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Wittenberger T., S
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Schaller H.C.,
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Sciurognathi;
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113;
   strategy
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                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                       Murinae;
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   succeeding
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D RECEPTORS.
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Best Local S
Matches 136
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Tr.

SEQUENCE 359 AA; 41462 MW; 2EB313C273EFCDEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the discovery of new g-protein country mol. Biol. 307:799-813(2001).
-!- SUBCELLULAR LOCATION: INTEGRALI-
-!- SIMILARITY: BELONGS TO FAMILY
EMBL; AF295366; AAK01866.1; -
MGD; MGI:1934133; GPF87.
PIAM; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BE53;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                              TISSUE-FRONTAL CORTEX;
Osada N., Hida M., Kusuda J., Tanuma F
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fascicularis (Crab eat
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BE53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn:
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae;
NCBI_TaxID=9541;
                                                                                                                               EMBL; AB056816; BAB39342.1; InterPro; IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                 Submitted (MAR-2001) to the
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                        libraries."
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les 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Macaca.
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41
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                                                                                                                                                                                                                                                                                                                                                                                                                          eating macaque) (Cynomolgus monkey).
sta; Craniata; Vertebrata; Euteleostomi;
tes; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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Last annotation update)
                                                                                                                                                                                 EMBL/GenBank/DDBJ
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Pred. No. 1.7e-53;
5; Mismatches 120;
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No. 1.7e-53;
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1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                           ₽.,
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                                                            UNKNOWN_1.
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                                                                                                                                                                                                                                 macaque
                                                                                                                                                                                      databases
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                 CRC64;
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                                                                                                                                                                                                                                   brain
                                                                                                                                                                                                                                                                                Hirai M.,
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                                                                                                                                                                                                                                                                                     Terao
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RESULT
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Best Local S
Matches 105
                                                                                           Query Match 31.1
Best Local Similarity 42.5
Matches 111; Conservative
                                                                                                                                                                                                                                  Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AF345566; AAK29069-1; -.
EMBL; BE009540; AAH09540.1: -.
                                                                                                                                                    EMBL; AR345566; ARK9069.1; -.

EMBL; BC009540; AAH09540.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PR00001; 7tm.1; 1.

PRINTS; PR00237; GPCRRHODDPSN.

PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Tracepter Coupled AA; 31443 MW; 1E7D498EE20717F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19, PUTATIVE G-PROTEIN-COUPLED R
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-LUNG CARCINOMA,
                                                                                                                                                                                                                                                                                                                                                   coupled receptor.";
Submitted (FEB-2001)
                                                                                                                                                                                                                                                                                                                                                                       Wang Y.-g, Gong L.;
"Identification of FKSG78, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          о9вхс2;
                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BXC2
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                         133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 46.7 nes 105; Conservative
 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                            MYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQP 167
SRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGVKWHTAVTY
           SNPKNLLGAKILSVVIWAFMFLLSLPNMILTNROPRDKNVKKCSFLKSEFGLVWHEIVNY 192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKNNKKLEGKVFVVVAVFFVCFAPFHFTRVPYTYSQTNNKTDCRLQNQLFTAKETTLFLA
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                                                                                                        31.1%;
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, Last sequence update)
, Last annotation updat
, RECEPTOR FKSG78 (G PRO
                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 559; DB 6; Length 228; Pred. No. 2.2e-42; 0; Mismatches 78; Indels
                                                                                             Score 553.5; DB 4;
Pred. No. 8.2e-42;
0; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                         novel gene encoding a putative
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Catarrhini; Hominidae
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(G PROTEIN-COUPLED
                                                                                                                                                                                                                                                                                                                                                     databases
                                                                                                                 Length
                                                                                              Indels
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                                                                                                                                                                   Transmembrane
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RESULT
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Best Local S
Matches 81
                                                                                         Q9TTY5;

Q1-MAY-2000 (TrEMBLrel. 13,

Q1-MAR-2001 (TrEMBLrel. 16,

Q1-DEC-2001 (TrEMBLrel. 19,

PLATELET-ACTIVATING FACTOR!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BY61 PRELIMINARY; PRT; 1/6 AA.
Q9BY61;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
SEQUENCE FROM N.A
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Boyldae; Boylnae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Zhang W., Wan T., Cao X.;
Zhang W., Wan T., Cao X.;
"Molecular cloning of a probable G protein-cou
transmembrane domains.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
EMBL; AF178982; AAK18752.1; -.
                                                                                                                                                         Q9TTY5
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HOMO Sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Ve;
Mammmalia; Eutheria; Primates; Catarrhini; I
                                                                      Bos taurus (Bovine).
                                                                                    PAFR.
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Pfam; PF00001; 7tm_1; 1
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                         PRELIMINARY;
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Last annotation updat
RECEPTOR.
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Pred.
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No. 1.
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les 57;
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                                                          Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF187321; AAF01139.2; -.
EMBL; AJ295321; CAC43290.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PFAm; PF00001; 7tm_1; 1.
PROSITE; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang W.S., Diehl J.R., Roudebush W.E.;
"Partial Sequence of Bovine Platelet-Activating Factor Receptor Gene.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular characterization of bovine platelet-actvating factor receptor transcripts and their detection in different tissues of cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        He B., Tiem Schmidt P.;
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                                                                                                                                                                                                                                                                                        121 RPIKTAQATTRKRGILLSLIIWVSIVGAASYFFVLD----STNREPNKTGSANITRC-F 174
                                                                                                                  298 YFFLCKSFRNSLISML-----KCPNSATS 321
                                                                                                                                                     234 VCTVLAVFIICFVPHHLVQLPWTLAEL-GFQDTDFHQAINDAHQVTLCLLSTNCVLDPII 292
                                                                                                                                                                                                                                                                                                                                                        YCFLTKKFRKHLTEKLYSMRESRKC-SRATS 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tiemann U., Kanitz W., Weikard R., Laurent P., Schwerin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 AA; 39691 MW; 7C4236205AE937C9 CRC64;
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                2002, 15:34:20
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Minimum
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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28, Appl
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US-08-852-824-2
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Sequence 61, Appl	Sequence 61, Appl	Sequence 61, Appl	-		•	•	Sequence 2, Appli	-	•	•	-	Sequence 2, Appli	•	•	Sequence 44, Appl	Sequence 3, Appli	Sequence 44, Appl

ALIGNMENTS

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Sequence 2, Application US/0885282
Patent NO. 6060272
Patent NO. 6060272
GENERAL INFORMATION:
APPLICANT: Li et al.
APPLICANT: Li et al.
APPLICANT: LO et al.
APPLICANT: LO et al.
CURRENT EFERENCE: 1488.1220000
CURRENT APPLICATION NUMBER: US/08
CURRENT ETLING DATE: 1997-05-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: genomic US-08-852-824-2
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 342; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                       1 MQAVDNLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI
                                                                                                                                                                                                                                                                  DRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKS
LCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM
                   LCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 342
                                                                                                                                                 EFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFI
                                                                                                                                  EFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFI
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Pred. No. 1.3e-144;
Mismatches 0;
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 342
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,456
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEAA81 RECEPTOR
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                        CPRDTRIVQLVEPALYTVVFLTGILLNTLALWVFVHIPSSSTFIIYLKNTLVADLIMTLM 74
NSATSLSQDNRKKEQD 332
                               VPYTHSQTNNKTDCRLQNQLFIAKETTLFLAATNICMDPLIYIFLCKKFTEKLPCMQ--G 312
                                                            IPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLISMLKCP 316
                                                                                                                            IFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVPFHFAR 256
                                                                                                                                                            KPVFAKTVSIFIWFFLFFISLPNTILSNKEATPSSVKKCASLKGPLGLKWHQMVNNICQF 194
                                                                                                                                                                                                                          LPFKILSDSHLAPWQLRAFYCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRNIFLK 134
                                                                                           IFWTVFILMLVFYVVIAKKVYDSYRKSKSKDRKNNKKLEGKVFVVVAVFFVCFAPFHFAR
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amino acid
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SZEKERES, PHILIP
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O. Box 980
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                                                                                                                                                                                                                                                                                                                                                   57; Mismatches 103;
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; Patent No. 5955303
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Best Local
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                                                                                             GENERAL INFORMATION:
APPLICANT: Au-You
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 CORRESPONDENCE ADDRESS:
                  NUMBER OF SEQUENCES:
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 333
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PRIOR APPLICATION NUMBER: 09/221,456
PRIOR FILING DATE: 1998-12-28
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APPLICANT: SZEKERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANYAGONISTS OF THE HNEAAB1 RECEPTOR
FILE REFERENCE: GH-70318-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/956,975
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TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE TITLE OF INVENTION: PROTEIN
                                                       APPLICANT: Guegler, Kar APPLICANT: Muzong Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 KPVFAKTVSIFIWFFLFFISLPNTILSNKEATPSSVKKCASLKGPLGLKWHQMVNNICQF 194
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5. 6358695
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                                                                                                                                                                                                  Application US/08812871
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                                                                                  Au-Young, Janice
Guegler, Karl
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STREET: 3174 POI CITY: Palo Alto STATE: CA

ADDRESSEE:

E: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.

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                                                                                                            RESULT
                                  Sequence 29, Application US/08467948A Patent No. 5998164 GENERAL INFORMATION:
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44.8%; Score 797; DB 2; Length 333;

Best Local Similarity 47.8%; Pred. No. 7.7e-61;

Matches 151; Conservative 57; Mismatches 106; Indels
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INFORMATION FOR SEQ ID NO: 1:
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IMMEDIATE SOURCE:
LIBRARY: MMLR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
APPLICANT:
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                    257 IPYTLSOTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLISMLKCP 316
                                                                                                                                                                                                                                                                                                                 195
                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                                                                                                                                               313 RKTTASSQENHSSQTD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 LPFKILSDSHLAPWQLRAFYCRESSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRNIFLK 134
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                                                                                                                                                                                                                                                                                                                                                                                                     NLLGAKILSVVIWAFMELLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEIVNYICQV 196
                                                                                                                                                                                               NSATSLSQDNRKKEQD 332
                                                                                                                                                                                                                                                                                                                                                                                  KPVFAKTVSIFIWFFLFFISLPIMILSNKEATPSSVKKCASLKGPLGLKWHQMVNNICQF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
                                                                                                                                                                                                                                   VPYTHSQTNNKTDCRLQNQLFIAKETTLFLAATNICMDPLISIFLCKKFTEKLPCMQ--G 312
                                                                                                                                                                                                                                                                                                                                              IFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVPFHFAR 256
                                                                                                                                                                                                                                                                                                            IFWTVLILMLVFYVVIAKKVYDSYRKSKCKDRKNNKKLEGKVFVVVPVFFVCFAPFHFAR 254
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CAO, LIANG
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US-08-467-948A-29
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Best Local :
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APPLICANT:
APPLICANT:
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LENGTH: 325 amino acid
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TELECOMMUNICATION INFORMATION: 202-371-2600
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ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
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APPLICATION NUMBER:
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MEDIUM TYPE: FLOPPY DISK
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                                                                                                 246 FICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSF
                                                                                                                                                    182 WHKASNYIFVAIFWIVFLLLIVFYTAITKKIFKSHLKSSRNSTSVKKKSSRNIFSIVFVF
                                                                                                                                                                                                                                 122 IVKPLWTSFIQSVSYSKLLSVIVWMLMLLLAVPNIILTNQSVREVTQIKCIELKSELGRK 181
                                                                                                                                                                                                                                                                   126 TTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLV 185
                                                                                                                                                                                                                                                                                                          66 TVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/467,948A FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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REILCKKLHIPLKA 315
                                    RNSLISMLKCPNSA 319
                                                                                                                                                                          WHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVF
                                                                           FVCFVPYHIARIPYTKSQTEAHYSCQSKEILRYMKEFTLLLSAANVCLDPIIYFFLCQPF
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149; Conserv
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.4%; Score 772; DB 2
47.5%; Pred. No. 1e-58;
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Best Local Similarity
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GENERAL II
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                                                                                                                                                                                                                                                                                                                                          Matches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS: LENGTH: 325 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT//
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
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                    246
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                                                                                                                                                                                                                  66 TVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                             62 IVIADEVMSLTEPEKILGDSGLGPWQLNVEVCRVSAVLEYVNMYVSIVEFGLISEDRYYK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                              TTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLV 185
                  FICEVPEHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSF 305
                                                     WHKASNYIFVAIFWIVELLLIVEYTAITKKIFKSHLKSSRNSTSVKKKSSRNIFSIVFVF
                                                                                      WHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVF 245
                                                                                                                         IVKPLWTSFIQSVSYSKLLSVIVWMLMLLLAVPNIILTNQSVREVTQIKCIELKSELGRK 181
                                                                                                                                                                                                                                                                    NSTSTQPPDESCSQNLLITQQIIPVLYCMVFIAGILLNGVSGWIFFYVPSSKSFIIYLKN 61
INFORMATION:
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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105; Indels
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US-08-988-876-8
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                                                                                                                                                                                          Best Local Similarity Matches 149; Conserv.
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J. REGISTRATION NUMBER: 36. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON OPERATING SYSTEM:
                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: Herewi
                                                                                          66 TVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQK 125
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                          6 NLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLKN 65
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IVKPLWTSFIQSVSYSKLLSVIVWMLMLLLAVPNIILTNQSVREVTQIKCIELKSELGRK 182
                                                                                                                         IVIADEVMSLTEPEKILGDSGLGPWQLNVFVCRVSAVLEYVNMYVSIVFFGLISFDRYYK 122
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3174 Porter Drive
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Best Local Similarity 47.5
Matches 149; Conservative
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PRIOR STLING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FRACE:
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APPLICANT: FOLEY, JIM

APPLICANT: FOLEY, JIM

APPLICANT: ARNOLD, ANNE ROMANIC

TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND

TITLE OF INVENTION: ANTAGONISTS OF THE INVERACTION BETWEEN THE HUMAN KIAAOOO1

TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
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                                                                                                                                           183 WHKASNYIFVAIFWIVFLLLIVFYTAITKKIFKSHLKSSRNSTSVKKKSSRNIFSIVFVF
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                                 RNSLISMLKCPNSA 319
                                                                                        FICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSB, 305
                                                                                                                                                                WHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVF 245
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                                                                FVCFVPYHIARIPYTKSQTEAHYSCQSKEILRYMKEFTLLLSAANVCLOPIIYFFLCQPF -302
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REILCKKLHIPLKA 316
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Best Local Similarity
Matches 132; Conserv
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APPLICANT: Lal, P
APPLICANT: Bandma
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MEDIUM TYPE: Diskett
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CTTY: Palo Alto
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CLONE: 1650519
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TOPOLOGY: lir
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REGISTRATION NUMBER: 30
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version
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VYFTCFLPYHLCRMPSTFSHLDRLLDESAQKILYYCKEITLFLSACNVCLDPIIYFFMCR
                                                           KWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKS--SRQFISQSSRKRKHNQSIRVVVA
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Hillman, Jennifer
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Best Local S
Matches 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/I
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS: LENGTH: 293 amino acid
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                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SUTTON III, GRANGER G. APPLICANT: ROSEN, CRAIG A. TITLE OF INVENTION: Polypucleotid TITLE OF INVENTION: Coupled Recep
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                      77 FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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No. 5998164
                                                                                                                                                     CTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLLMILT 76
IFWINELIVIVCYTLITKE----LYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVP-
                              KPVWGKTVSIFIWFFWFFISLPNMILSNKEATPSSVKKCASLKGPLGLKWHQMVNNICQF 194
                                                           NLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEIVNYICQV 196
                                                                                         LPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRNIFLK 134
                                                                                                                                                                                                                   al Similarity
116; Conserv
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                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                           293 amino acids
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BULT, CAROL J.
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                   30.7%; Score 546.5;
42.3%; Pred. No. 1.70
tive 45; Mismatches
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                                                                                                                                                                                                                                1.7e-39;
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                                                                                                                                                                                                       Matches 116;
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INFORMATION FOR SEQ
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FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein TITLE OF INVENTION: Coupled Receptor GPR1 NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                               137 NLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEIVNYICQV 196
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                                                                                                                                                      TYPE: amino acid
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REGISTRATION NUMBER:
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SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
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                                                                   75 LPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRNIFLK 134
                                                                                                                                    15 CPKDTRIVQLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIIYLKNTLVADLIMTLM 74
                                                                                                                                                                                                                         Local Similarity
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No. 6090575
                                                                                                  FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
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KPVWGKTVSIFIWFFWFFISLPNMILSNKEATPSSVKKCASLKGPLGLKWHQMVNNICQF 194
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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CAO, L
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06-JUN-1995
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                                                                                                                                                                                                                     30.7%; Score 546.5; DB 3 42.3%; Pred. No. 1.7e-39;
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Best Local Similarity
Matches 112; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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120 CKIYRIQEPGFAKMISTVVWLMVLLIMVPNMMIPIKDIKEKSNVGCMEFKKEFGRNWHLL 179
                           130 FKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEI 189
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                                                                                                                                                     13 NTSLCTRDYKITQVLEPLLYTVLEFVGLITNGLAMRIFFQIRSKSNFI-IFLKNTVISDL 71
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                                                                                              LMILTEPEKILSDAKLGTGP--LRTEVCQVTSVIFYETMYISISFLGLITIDRYQKTTRP 129
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                                                             LLTLALPVKIVVD--LGVAPWKLKIFHCQVTACLIYINMYLSIIFLAFVSIDRCLQLTHS
                                                                                                                               NSSFFCPVYKDLEP-FTYFFYLVFLVGIIGSCFATWAFIQKNTNHRCVSIYLINLLTADF 61
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Treacy, Maurice
Spaulding, Vikki
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87 CambridgePark Drive
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                                                                                                                                                                                                                27.4%; Score 488; DB 1; Length 319; 34.5%; Pred. No. 1.8e-34;
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US-08-118-270-39
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                                                                                                                                                                              Best Loc
Matches
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                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 09-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Murphy, Randall B. APPLICANT: Schuster, David I.
                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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295
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                                                                                                                                                                                                                                                                                                                              TYPE:
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                                                                                                                                               27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                              SNQGNWFLPKFLCNLAGCLFFINTYCSVAFLGVITYNRFQAVKYPIKTAQATTRKRGIAL 120
                                                                                                                                 LFPLLYTVLFFVGLITNGLAMRIFFQI-RSKSNFI-IFLKNTVISDLLMILTFPFKILSD 84
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                                                                                                               LFPIVYSIIFVLGIIANGYVLWVFARLYPSKKNEIKIFMVNLTVADLLFLITLPLWIVYY 60
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                                                                               AKLGTGPLRTEVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
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                                                                                                                                                                                                                                                                                                                                           326 amino acids
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9 Seventh Street, N.W.,
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                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kevin
                                                                                                                                                                             23.1%; Score 410.5; DB 1; 32.2%; Pred. No. 7.7e-28; tive 65; Mismatches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version
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PCT-US93-08528-39
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Best Local Similarity
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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234 MVQLPWTLAEL-GMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFRKHLSEKL 292
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                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Townsend, Kevin REGISTRATION NUMBER: 3
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                                                 SNQGNWFLPKFLCNLAGCLFFINTYCSVAFLGVITYNRFQAVKYPIKTAQATTRKRGIAL 120
                                                                      AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
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                                                                                                                   LEPIVYSITEVLGITANGYVLWVFARLYPSKKNEIKIFMVNLTVADLLFLITLPLWIVYY 60
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                           326 amino acids
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New York University
NENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
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                                                                                                                                                                                                    Score 410.5; DB 5
Pred. No. 7.7e-28;
                                                                                                                                                                                      Mismatches 137;
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                                                                                                                                                                                                                      DB 5;
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20 DYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQI--RSKSNFI-IFLKNTVISDLLMILT 76

DSEFRYTLFPIVYSIIFVLGIIANGYVLWVFARLYPSKKLNEIKIFMVNLTVADLLFLIT 69

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US-08-988-876-9
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                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                         ANTHURNEL, COLL.

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
                                                                                                                               TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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SOFTWARE: FastSE
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CITY: Palo Alto
                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                   TYPE:
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Hillman, Jennifer L.
 Conservative
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                 Score 392.5; DB 3; Pred. No. 2.8e-26;
   Mismatches
                                  Length
 Indels
 21;
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